

SEQUENCE LISTING

<110> Jones, Brian E

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P-3

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Sadlowski, E.

Shaw, Andrew

van der Kleij. Wilhelmus 11

van Marrenwijk Lee

<120> Serine Proteases, Nucleic Acids Encoding Serine Enzymes and Vectors and Host Cells Incorporating Same

<130> GC819-2-US/B

<140> US 10/576 331

<141> 2004-11-18

<150> PCT/US2001/038855

<151> 2004-11-10

<150> US 60/533, see

<150> 05 60/523,
<151> 3003 11 12

<160> 656

<170> PatentIn version 2.0

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≤211> 1680

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<212> RNA

<212> DNA
<213> Cellulose

1400-1

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<212> DNA
<213> Cellulomonas strain 69B4

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<212> DNA
<213> Cellulomonas spp.

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gccgaccc	aggcctggaa	gaccgtc	gacgcggccc	tcgagg	cgacgacgt	360
cccaccc	acgtcgacgt	cccgaccaac	agcgtcg	tcgccc	ggccggagcc	420
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ggccactgcg	ccgcacccgg	cgccaccacc	gccaacccca	ccgggac	cgccgggtcc	660

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<210> 4
<211> 567
<212> DNA
<213> *Cellulomonas* spp.

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accgtcccg	gcctgatccg	caccaccgtc	tgcgccgagc	ccggcgactc	cggtgtggctcg			420
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<210> 5
<211> 83
<212> DNA
<213> Cellulomonas strain 69B4

<400> 5
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<210> 6
<211> 495
<212> PRT
<213> Cellulomonas strain 69B4

<400> 6

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Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala	Asn	Glu	Pro	Ala
							20			25			30		
Pro	Pro	Gly	Ser	Ala	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Glu	Lys	Leu	Asp
							35		40			45			
Pro	Asp	Leu	Leu	Glu	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Asp	Ala	Glu
						50			55		60				
Glu	Ala	Ala	Ala	Thr	Leu	Ala	Phe	Gln	His	Asp	Ala	Ala	Glu	Thr	Gly
65						70				75			80		

Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr Trp Val
 85 90 95
 Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala Val Glu
 100 105 110
 Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His Ser Leu
 115 120 125
 Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu Glu Gly
 130 135 140
 His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn Ser Val
 145 150 155 160
 Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly Leu Val
 165 170 175
 Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu Thr Asp
 180 185 190
 Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
 195 200 205
 Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn Gly Gly
 210 215 220
 Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn
 225 230 235 240
 Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
 245 250 255
 Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val Asn Asn
 260 265 270
 Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala Pro Val
 275 280 285
 Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
 290 295 300
 Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly Thr Val
 305 310 315 320
 Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
 325 330 335
 Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly
 340 345 350
 Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Asn
 355 360 365
 Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr Thr Asp Ser Gly
 370 375 380
 Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly Tyr Ala Arg Thr
 385 390 395 400
 Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala Gln Pro Asn Gly
 405 410 415
 Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser Val Cys Leu Asn
 420 425 430
 Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln Arg Trp Asn Gly
 435 440 445
 Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro Gly Ser Asn Glu
 450 455 460
 Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg Tyr Val Val Asn
 465 470 475 480
 Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu Thr Leu Pro
 485 490 495

<210> 7
 <211> 467
 <212> PRT
 <213> Cellulomonas strain 69B4

Asn Glu Pro Ala Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala
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 Glu Lys Leu Asp Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly
 20 25 30
 Leu Asp Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala
 35 40 45
 Ala Glu Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala
 50 55 60
 Gly Thr Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu
 65 70 75 80
 Asp Ala Val Glu Glu Val Glu Gly Glu Ala Thr Ala Val Thr Val
 85 90 95
 Glu His Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala
 100 105 110
 Ala Leu Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro
 115 120 125
 Thr Asn Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala
 130 135 140
 Ala Gly Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe
 145 150 155 160
 Val Glu Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly
 165 170 175
 Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala
 180 185 190
 Val Asn Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala
 195 200 205
 Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly
 210 215 220
 Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
 225 230 235 240
 Gln Val Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr
 245 250 255
 Ala Ala Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly
 260 265 270
 Trp His Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro
 275 280 285
 Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro
 290 295 300
 Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val
 305 310 315 320
 Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe
 325 330 335
 Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr
 340 345 350
 Thr Asp Ser Gly Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly
 355 360 365
 Tyr Ala Arg Thr Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala
 370 375 380
 Gln Pro Asn Gly Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser
 385 390 395 400
 Val Cys Leu Asn Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln
 405 410 415
 Arg Trp Asn Gly Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro
 420 425 430

Gly Ser Asn Glu Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg
435 440 445
Tyr Val Val Asn Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu
450 455 460
Thr Leu Pro
465

<210> 8
<211> 189
<212> PRT
<213> Cellulomonas spp.

<400> 8

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Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
20 25 30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
35 40 45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
50 55 60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
65 70 75 80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
85 90 95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
100 105 110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
115 120 125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Ser Leu Leu Ala Gly
130 135 140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145 150 155 160
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
165 170 175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
180 185

<210> 9
<211> 28
<212> PRT
<213> Cellulomonas strain 69B4

<400> 9

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
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Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
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<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

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<222> (3)..(3)
<223> n is a, c, g, or t

<400> 10
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<210> 11
<211> 19
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<213> Artificial Sequence

<220>
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<222> (2)..(17)
<223> n is a, c, g, or t

<400> 11
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<210> 12
<211> 58
<212> PRT
<213> Cellulomonas strain 69B4

<400> 12

Asp Gly Trp Asp Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr
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Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala
20          25          30
Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln
35          40          45
Gly Val Thr Ser Gly Asp Ser Gly Gly Ser
50          55

<210> 13
<211> 177
<212> DNA
<213> Cellulomonas strain 69B4

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<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

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<220>
<223> primer

<400> 14
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<210> 15
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
gctcgccggc aaccaggccc agggcgtaac gtc 33

<210> 16
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<213> Artificial Sequence

<220>
<223> primer

<400> 16
aacggcggtt tcatcacccgc cggccactgc ggcc 34

<210> 17
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminus of the mature chain determined by MALDI-TOF analysis

<400> 17

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1 5 10 15

<210> 18
<211> 189
<212> PRT
<213> Cellulomonas strain 69B4

<400> 18

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
1 5 10 15
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
20 25 30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
35 40 45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala

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Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg		80
85	90	95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn		
100	105	110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr		
115	120	125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly		
130	135	140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr		
145	150	155
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr		160
165	170	175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro		
180	185	

<210> 19

<211> 184

<212> PRT

<213> Streptomyces griseus

<400> 19

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Thr Ala Gly His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr		
35	40	45
Arg Thr Gly Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His		
50	55	60
Ser Asn Pro Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser		
65	70	75
Tyr Gln Asp Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val		80
85	90	95
Gln Arg Ser Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly		
100	105	110
Leu Asn Ala Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met		
115	120	125
Ile Gln Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu		
130	135	140
Phe Ala Gly Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn		
145	150	155
Cys Arg Thr Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu		160
165	170	175
Ser Ala Tyr Gly Ala Thr Val Leu		
180		

<210> 20

<211> 174

<212> PRT

<213> Streptomyces fradiae

<400> 20

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Ala Gly His Cys Thr Glu Ile Ala Ser Thr Trp Tyr Thr Asn Ser Gly
35 40 45
Gln Thr Ser Leu Leu Gly Thr Arg Ala Gly Thr Ser Phe Pro Gly Asn
50 55 60
Asp Tyr Gly Leu Ile Arg His Ser Asn Ala Ser Ala Ala Asp Gly Arg
65 70 75 80
Val Tyr Leu Tyr Asn Gly Ser Tyr Arg Asp Ile Thr Gly Ala Gly Asn
85 90 95
Ala Tyr Val Gly Gln Thr Val Gln Arg Ser Gly Ser Thr Thr Gly Leu
100 105 110
His Ser Gly Arg Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly
115 120 125
Gly Asp Ile Val Ser Gly Leu Ile Gln Thr Asn Val Cys Ala Glu Pro
130 135 140
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Ser Thr Ala Leu Gly Leu
145 150 155 160
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr
165 170

<210> 21
<211> 188
<212> PRT
<213> Streptomyces lividans

<400> 21

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20 25 30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser
35 40 45
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly
50 55 60
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly
65 70 75 80
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly
85 90 95
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg
100 105 110
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val Val
115 120 125
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
130 135 140
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly
145 150 155 160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
165 170 175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
180 185

<210> 22
<211> 188

<212> PRT

<213> Streptomyces coelicolor

<400> 22

Asn Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Arg Thr Ser Ser Gly Ala Glu Tyr Phe
20 25 30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser
35 40 45
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly
50 55 60
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly
65 70 75 80
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly
85 90 95
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg
100 105 110
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val Val
115 120 125
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
130 135 140
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly
145 150 155 160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
165 170 175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
180 185

<210> 23

<211> 189

<212> PRT

<213> Streptomyces albogriseolus

<400> 23

Thr Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Val Asp Tyr Phe
20 25 30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Thr Trp Tyr Ser Asn
35 40 45
Ser Ala Arg Thr Thr Ala Ile Gly Ser Thr Ala Gly Ser Ser Phe Pro
50 55 60
Gly Asn Asp Tyr Gly Ile Val Arg Tyr Thr Gly Ser Val Ser Arg Pro
65 70 75 80
Gly Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val
85 90 95
Gly Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly
100 105 110
Arg Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Ile
115 120 125
Val Ser Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser
130 135 140
Gly Gly Pro Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser

145 150 155 160
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro
 165 170 175
Val Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
 180 185

<210> 24
<211> 188
<212> PRT
<213> Streptomyces griseus

<400> 24

Thr Lys Leu Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu
 20 25 30
Thr Ala Gly His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser
 35 40 45
Ala Arg Thr Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn
 50 55 60
Asn Asp Tyr Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp
65 70 75 80
Gly Thr Val Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val
 85 90 95
Gly Met Ala Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly
 100 105 110
Ser Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val
 115 120 125
Val Tyr Gly Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser
130 135 140
Gly Gly Pro Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly
145 150 155 160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
 165 170 175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
 180 185

<210> 25
<211> 188
<212> PRT
<213> Streptomyces griseus

<400> 25

Val Leu Gly Gly Ala Ile Tyr Gly Gly Ser Arg Cys Ser Ala
1 5 10 15
Ala Phe Asn Val Thr Lys Gly Gly Ala Arg Tyr Phe Val Thr Ala Gly
 20 25 30
His Cys Thr Asn Ile Ser Ala Asn Trp Ser Ala Ser Ser Gly Gly Ser
 35 40 45
Val Val Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn Asp Tyr Gly
 50 55 60
Ile Val Arg Tyr Thr Asp Gly Ser Ser Pro Ala Gly Thr Val Asp Leu
65 70 75 80
Tyr Asn Gly Ser Thr Gln Asp Ile Ser Ser Ala Ala Asn Ala Val Val
 85 90 95

Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly
100 105 110
Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val
115 120 125
Tyr Asn Met Gly Arg Thr Thr Ala Cys Ser Ala Gly Gly Asp Ser Gly
130 135 140
Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His Ser Gly Ser
145 150 155 160
Ser Gly Cys Ser Gly Thr Ala Gly Ser Ala Ile His Gln Pro Val Thr
165 170 175
Lys Ala Leu Ser Ala Tyr Gly Val Thr Val Tyr Leu
180 185

<210> 26
<211> 190
<212> PRT
<213> Streptomyces fradiae

<400> 26

Gln Arg Glu Val Ala Gly Gly Asp Ala Ile Tyr Gly Gly Ser Arg
1 5 10 15
Cys Ser Ala Ala Phe Asn Val Thr Lys Asn Gly Val Arg Tyr Phe Leu
20 25 30
Thr Ala Gly His Cys Thr Asn Leu Ser Ser Thr Trp Ser Ser Thr Ser
35 40 45
Gly Gly Thr Ser Ile Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn
50 55 60
Asp Tyr Gly Ile Val Arg Tyr Thr Thr Thr Asn Val Asp Gly Arg
65 70 75 80
Val Asn Leu Tyr Asn Gly Gly Tyr Gln Asp Ile Ala Ser Ala Ala Asp
85 90 95
Ala Val Val Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val
100 105 110
Thr Ser Gly Thr Val Ser Ala Val Asn Val Thr Val Asn Tyr Ser Asp
115 120 125
Gly Pro Val Tyr Gly Met Val Arg Thr Thr Ala Cys Ser Ala Gly Gly
130 135 140
Asp Ser Gly Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His
145 150 155 160
Ser Gly Ser Ser Gly Cys Thr Gly Thr Asn Gly Ser Ala Ile His Gln
165 170 175
Pro Val Arg Glu Ala Leu Ser Ala Tyr Gly Val Asn Val Tyr
180 185 190

<210> 27
<211> 190
<212> PRT
<213> Streptomyces albogriseolus

<400> 27

Lys Pro Phe Ile Ala Gly Gly Asp Ala Ile Thr Gly Asn Gly Gly Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Thr Lys Gly Gly Glu Pro His Phe Leu
20 25 30
Thr Ala Gly His Cys Thr Glu Gly Ile Ser Thr Trp Ser Asp Ser Ser

35	40	45	
Gly Gln Val Ile Gly Glu Asn Ala Ala Ser Ser Phe Pro Gly Asp Asp			
50	55	60	
Tyr Gly Leu Val Lys Tyr Thr Ala Asp Val Ala His Pro Ser Gln Val			
65	70	75	80
Asn Leu Tyr Asp Gly Ser Ser Gln Ser Ile Ser Gly Ala Ala Glu Ala			
85	90	95	
Ala Val Gly Met Gln Val Thr Arg Ser Gly Ser Thr Thr Gln Val His			
100	105	110	
Ser Gly Thr Val Thr Gly Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly			
115	120	125	
Asp Ile Val Asn Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly			
130	135	140	
Asp Ser Gly Gly Ser Leu Phe Ser Gly Asp Lys Ala Val Gly Leu Thr			
145	150	155	160
Ser Gly Gly Ser Gly Asp Cys Thr Ser Gly Gly Thr Thr Phe Phe Gln			
165	170	175	
Pro Val Thr Glu Ala Leu Ser Ala Thr Gly Thr Gln Ile Gly			
180	185	190	

<210> 28
<211> 190
<212> PRT

<213> Streptomyces coelicolor

<400> 28

Lys Pro Phe Val Ala Gly Gly Asp Ala Ile Thr Gly Gly Gly Gly Arg			
1	5	10	15
Cys Ser Leu Gly Phe Asn Val Thr Lys Gly Gly Glu Pro Tyr Phe Ile			
20	25	30	
Thr Ala Gly His Cys Thr Glu Ser Ile Ser Thr Trp Ser Asp Ser Ser			
35	40	45	
Gly Asn Val Ile Gly Glu Asn Ala Ala Ser Ser Phe Pro Asp Asn Asp			
50	55	60	
Tyr Gly Leu Val Lys Tyr Thr Ala Asp Val Asp His Pro Ser Glu Val			
65	70	75	80
Asn Leu Tyr Asn Gly Ser Ser Gln Ala Ile Ser Gly Ala Ala Glu Ala			
85	90	95	
Thr Val Gly Met Gln Val Thr Arg Ser Gly Ser Thr Thr Gln Val His			
100	105	110	
Asp Gly Thr Val Thr Gly Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly			
115	120	125	
Asp Ile Val Asn Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly			
130	135	140	
Asp Ser Gly Gly Ser Leu Phe Ser Gly Asp Gln Ala Ile Gly Leu Thr			
145	150	155	160
Ser Gly Gly Ser Gly Asp Cys Thr Ser Gly Gly Glu Thr Phe Phe Gln			
165	170	175	
Pro Val Thr Glu Ala Leu Ser Ala Thr Gly Thr Gln Ile Gly			
180	185	190	

<210> 29
<211> 191
<212> PRT
<213> Streptomyces griseus

<400> 29

Thr Pro Leu Ile Ala Gly Gly Asp Ala Ile Trp Gly Ser Gly Ser Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Val Lys Gly Gly Glu Pro Tyr Phe Leu
20 25 30
Thr Ala Gly His Cys Thr Glu Ser Val Thr Ser Trp Ser Asp Thr Gln
35 40 45
Gly Gly Ser Glu Ile Gly Ala Asn Glu Gly Ser Ser Phe Pro Glu Asn
50 55 60
Asp Tyr Gly Leu Val Lys Tyr Thr Ser Asp Thr Ala His Pro Ser Glu
65 70 75 80
Val Asn Leu Tyr Asp Gly Ser Thr Gln Ala Ile Thr Gln Ala Gly Asp
85 90 95
Ala Thr Val Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val
100 105 110
His Asp Gly Glu Val Thr Ala Leu Asp Ala Thr Val Asn Tyr Gly Asn
115 120 125
Gly Asp Ile Val Asn Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro
130 135 140
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Asp Thr Ala Leu Gly Leu
145 150 155 160
Thr Ser Gly Gly Ser Gly Asp Cys Ser Ser Gly Gly Thr Thr Phe Phe
165 170 175
Gln Pro Val Pro Glu Ala Leu Ala Ala Tyr Gly Ala Glu Ile Gly
180 185 190

<210> 30

<211> 200

<212> PRT

<213> Streptomyces lividans

<400> 30

Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Gly Ala Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Ala Ala Phe
20 25 30
Leu Thr Arg Gly His Cys Gly Gly Ala Thr Met Trp Ser Asp Ala
35 40 45
Gln Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Pro
50 55 60
Glu Gly Asp Phe Gly Leu Val Arg Tyr Asp Gly Pro Ser Thr Glu Ala
65 70 75 80
Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala
85 90 95
Ala Glu Ala Ser Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr
100 105 110
Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Val Thr Val Asn Tyr
115 120 125
Pro Glu Gly Thr Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu
130 135 140
Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile
145 150 155 160
Arg Leu Thr Ser Gly Gly Thr Arg Asp Cys Thr Ser Gly Gly Glu Thr
165 170 175
Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Gly Thr Leu

180 185 190
Gly Gly Glu Asp Gly Gly Asp Gly
 195 200

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<210> 31
<211> 201
<212> PRT
<213> Streptomyces coelicolor
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<400> 31

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Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Gly Ala Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Pro Ala Phe
20 25 30
Leu Thr Ala Gly His Cys Gly Val Ala Ala Asp Gln Trp Ser Asp Ala
35 40 45
Gln Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Gly
50 55 60
Glu Gly Asp Phe Ala Leu Val Arg Tyr Asp Asp Pro Ala Thr Glu Ala
65 70 75 80
Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala
85 90 95
Ala Glu Ala Ala Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr
100 105 110
Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Ala Thr Val Asn Tyr
115 120 125
Pro Glu Gly Met Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu
130 135 140
Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile
145 150 155 160
Gly Leu Thr Ser Gly Gly Ser Gly Asp Cys Thr Val Gly Gly Glu Thr
165 170 175
Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Ala Thr Leu
180 185 190
Gly Gly Glu Asp Gly Gly Ala Gly Ala
195 200

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<210> 32
<211> 68
<212> PRT
<213> Streptomyces platensis

<400> 32

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Val Asp Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly Asp Ser
1           5           10          15
Gly Gly Ala Leu Phe Asp Gly Asp Ala Ala Ile Gly Leu Thr Ser Gly
20          25          30
Gly Ser Gly Asp Cys Ser Gln Gly Gly Glu Thr Phe Phe Gln Pro Val
35          40          45
Thr Glu Ala Leu Lys Ala Tyr Gly Ala Gln Ile Gly Gly Gln Gly
50          55          60
Glu Pro Pro Glu
65

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<210> 33

<211> 201
<212> PRT
<213> Streptomyces coelicolor

<400> 33

Thr Thr Arg Leu Asn Gly Ala Glu Pro Ile Leu Ser Thr Ala Gly Arg
1 5 10 15
Cys Ser Ala Gly Phe Asn Val Thr Asp Gly Thr Ser Asp Phe Ile Leu
20 25 30
Thr Ala Gly His Cys Gly Pro Thr Gly Ser Val Trp Phe Gly Asp Arg
35 40 45
Pro Gly Asp Gly Gln Val Gly Arg Thr Val Ala Gly Ser Phe Pro Gly
50 55 60
Asp Asp Phe Ser Leu Val Glu Tyr Ala Asn Gly Lys Ala Gly Asp Gly
65 70 75 80
Ala Asp Val Val Ala Val Gly Asp Gly Lys Gly Val Arg Ile Thr Gly
85 90 95
Ala Gly Glu Pro Ala Val Gly Gln Arg Val Phe Arg Ser Gly Ser Thr
100 105 110
Ser Gly Leu Arg Asp Gly Arg Val Thr Ala Leu Asp Ala Thr Val Asn
115 120 125
Tyr Pro Glu Gly Thr Val Thr Gly Leu Ile Glu Thr Asp Val Cys Ala
130 135 140
Glu Pro Gly Asp Ser Gly Gly Pro Met Phe Ser Glu Gly Val Ala Leu
145 150 155 160
Gly Val Thr Ser Gly Gly Ser Gly Asp Cys Ala Lys Gly Gly Thr Thr
165 170 175
Phe Phe Gln Pro Leu Pro Glu Ala Met Ala Ser Leu Gly Val Arg Leu
180 185 190
Ile Val Pro Gly Arg Glu Gly Ala Ala
195 200

<210> 34
<211> 188
<212> PRT
<213> Metarhizium anisopliae

<400> 34

Ala Thr Val Gln Gly Gly Asp Val Tyr Tyr Ile Asn Arg Ser Ser Arg
1 5 10 15
Cys Ser Ile Gly Phe Ala Val Thr Thr Gly Phe Val Ser Ala Gly His
20 25 30
Cys Gly Gly Ser Gly Ala Ser Ala Thr Thr Ser Ser Gly Glu Ala Leu
35 40 45
Gly Thr Phe Ser Gly Ser Val Phe Pro Gly Ser Ala Asp Met Ala Tyr
50 55 60
Val Arg Thr Val Ser Gly Thr Val Leu Arg Gly Tyr Ile Asn Gly Tyr
65 70 75 80
Gly Gln Gly Ser Phe Pro Val Ser Gly Ser Ser Glu Ala Ala Val Gly
85 90 95
Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gln Val His Cys Gly Thr
100 105 110
Ile Gly Ala Lys Gly Ala Thr Val Asn Tyr Pro Gln Gly Ala Val Ser
115 120 125
Gly Leu Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly

130	135	140
Ser Phe Tyr Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser		
145	150	155
Gly Asp Cys Ser Arg Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Arg		160
	165	170
Ile Leu Gln Thr Tyr Gly Leu Thr Leu Val Thr Ala		175
	180	185

<210> 35
<211> 195
<212> PRT
<213> *Streptomyces griseus*

<400> 35

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg		
1	5	10
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala		
	20	25
Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Thr Asn Gly Val Asn		
	35	40
Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp		
	50	55
Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val		
	65	70
Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser		
	85	90
Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His		
	100	105
Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly		
	115	120
Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp		
	130	135
Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser		
	145	150
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro		
	165	170
Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly		
	180	185
Gly Gly Thr		190
	195	

<210> 36
<211> 197
<212> PRT
<213> *Streptomyces coelicolor*

<400> 36

Tyr Asp Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg		
1	5	10
Cys Ser Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala		
	20	25
Thr Ala Gly His Cys Gly Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn		
	35	40
Arg Val Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp		
	50	55
		60

Met Ala Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val
65 70 75 80
Leu Gly Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser
85 90 95
Pro Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
100 105 110
Cys Gly Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly
115 120 125
Thr Ile Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp
130 135 140
Ser Gly Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser
145 150 155 160
Gly Gly Ser Gly Asp Cys Arg Thr Gly Gly Glu Thr Phe Phe Gln Pro
165 170 175
Ile Asn Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly
180 185 190
Gly Asp Asp Gly Gly
195

<210> 37
<211> 189
<212> PRT
<213> Streptomyces spp.

<400> 37

Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Ile Gly Asn Gly Arg Cys
1 5 10 15
Ser Ile Gly Phe Ser Val Arg Gln Gly Ser Thr Pro Gly Phe Val Thr
20 25 30
Ala Gly His Cys Gly Ser Val Gly Asn Ala Thr Thr Gly Phe Asn Arg
35 40 45
Val Ser Gln Gly Thr Phe Arg Gly Ser Trp Phe Pro Gly Arg Asp Met
50 55 60
Ala Trp Val Ala Val Asn Ser Asn Trp Thr Pro Thr Ser Leu Val Arg
65 70 75 80
Asn Ser Gly Ser Gly Val Arg Val Thr Gly Ser Thr Gln Ala Thr Val
85 90 95
Gly Ser Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly
100 105 110
Thr Ile Gln Gln His Asn Thr Ser Val Thr Tyr Pro Gln Gly Thr Ile
115 120 125
Thr Gly Val Thr Arg Thr Ser Ala Cys Ala Gln Pro Gly Asp Ser Gly
130 135 140
Gly Ser Phe Ile Ser Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly
145 150 155 160
Ser Gly Asn Cys Ser Ile Gly Gly Thr Thr Phe His Gln Pro Val Asn
165 170 175
Pro Ile Leu Ser Gln Tyr Gly Leu Thr Leu Val Arg Ser
180 185

<210> 38
<211> 187
<212> PRT
<213> Streptomyces spp.

<400> 38

Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Met Gly Gly Gly Arg Cys
 1 5 10 15
 Ser Val Gly Phe Ser Val Thr Gln Gly Ser Thr Pro Gly Phe Ala Thr
 20 25 30
 Ala Gly His Cys Gly Thr Val Gly Thr Ser Thr Thr Gly Tyr Asn Gln
 35 40 45
 Ala Ala Gln Gly Thr Phe Glu Glu Ser Ser Phe Pro Gly Asp Asp Met
 50 55 60
 Ala Trp Val Ser Val Asn Ser Asp Trp Asn Thr Thr Pro Thr Val Asn
 65 70 75 80
 Glu Gly Glu Val Thr Val Ser Gly Ser Thr Glu Ala Ala Val Gly Ala
 85 90 95
 Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile
 100 105 110
 Gln Gln His Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr Ile Thr Gly
 115 120 125
 Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser
 130 135 140
 Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly
 145 150 155 160
 Asn Cys Thr Ser Gly Gly Thr Thr Tyr His Gln Pro Ile Asn Pro Leu
 165 170 175
 Leu Ser Ala Tyr Gly Leu Asp Leu Val Thr Gly
 180 185

<210> 39
 <211> 193
 <212> PRT
 <213> Streptomyces coelicolor

<400> 39

Glu Asp Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg
 1 5 10 15
 Cys Ser Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala
 20 25 30
 Thr Ala Gly His Cys Gly Asp Pro Gly Ala Thr Thr Gly Tyr Asn
 35 40 45
 Glu Ala Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp
 50 55 60
 Met Ala Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val
 65 70 75 80
 Lys Ala Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala
 85 90 95
 Leu Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
 100 105 110
 Cys Gly Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly
 115 120 125
 Thr Val Asp Gly Leu Thr Glu Thr Thr Val Cys Ala Glu Pro Gly Asp
 130 135 140
 Ser Gly Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser
 145 150 155 160
 Gly Gly Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro
 165 170 175
 Val Asn Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser
 180 185 190

Ala

<210> 40
<211> 187
<212> PRT
<213> Thermobifida fusca

<400> 40

Leu Ala Ala Ile Ile Gly Gly Asn Pro Tyr Tyr Phe Gly Asn Tyr Arg
1 5 10 15
Cys Ser Ile Gly Phe Ser Val Arg Gln Gly Ser Gln Thr Gly Phe Ala
20 25 30
Thr Ala Gly His Cys Gly Ser Thr Gly Thr Arg Val Ser Ser Pro Ser
35 40 45
Gly Thr Val Ala Gly Ser Tyr Phe Pro Gly Arg Asp Met Gly Trp Val
50 55 60
Arg Ile Thr Ser Ala Asp Thr Val Thr Pro Leu Val Asn Arg Tyr Asn
65 70 75 80
Gly Gly Thr Val Thr Val Thr Gly Ser Gln Glu Ala Ala Thr Gly Ser
85 90 95
Ser Val Cys Arg Ser Gly Ala Thr Thr Gly Trp Arg Cys Gly Thr Ile
100 105 110
Gln Ser Lys Asn Gln Thr Val Arg Tyr Ala Glu Gly Thr Val Thr Gly
115 120 125
Leu Thr Arg Thr Thr Ala Cys Ala Glu Gly Asp Ser Gly Gly Pro
130 135 140
Trp Leu Thr Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Thr Gly
145 150 155 160
Asp Cys Arg Ser Gly Gly Ile Thr Phe Phe Gln Pro Ile Asn Pro Leu
165 170 175
Leu Ser Tyr Phe Gly Leu Gln Leu Val Thr Gly
180 185

<210> 41
<211> 198
<212> PRT
<213> Lysobacter enzymogenes

<400> 41

Ala Asn Ile Val Gly Gly Ile Glu Tyr Ser Ile Asn Asn Ala Ser Leu
1 5 10 15
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Ala Thr Lys Gly Phe Val
20 25 30
Thr Ala Gly His Cys Gly Thr Val Asn Ala Thr Ala Arg Ile Gly Gly
35 40 45
Ala Val Val Gly Thr Phe Ala Ala Arg Val Phe Pro Gly Asn Asp Arg
50 55 60
Ala Trp Val Ser Leu Thr Ser Ala Gln Thr Leu Leu Pro Arg Val Ala
65 70 75 80
Asn Gly Ser Ser Phe Val Thr Val Arg Gly Ser Thr Glu Ala Ala Val
85 90 95
Gly Ala Ala Val Cys Arg Ser Gly Arg Thr Thr Gly Tyr Gln Cys Gly
100 105 110
Thr Ile Thr Ala Lys Asn Val Thr Ala Asn Tyr Ala Glu Gly Ala Val

115	120	125
Arg Gly Leu Thr Gln Gly Asn Ala Cys Met Gly Arg Gly Asp Ser Gly		
130	135	140
Gly Ser Trp Ile Thr Ser Ala Gly Gln Ala Gln Gly Val Met Ser Gly		
145	150	155
Gly Asn Val Gln Ser Asn Gly Asn Asn Cys Gly Ile Pro Ala Ser Gln		
165	170	175
Arg Ser Ser Leu Phe Glu Arg Leu Gln Pro Ile Leu Ser Gln Tyr Gly		
180	185	190
Leu Ser Leu Val Thr Gly		
195		

<210> 42
<211> 189
<212> PRT
<213> Streptomyces coelicolor

<400> 42

Ala Ala Gly Thr Val Gly Gly Asp Pro Tyr Tyr Thr Gly Asn Val Arg			
1	5	10	15
Cys Ser Ile Gly Phe Ser Val His Gly Gly Phe Val Thr Ala Gly His			
20	25	30	
Cys Gly Arg Ala Gly Ala Gly Val Ser Gly Trp Asp Arg Ser Tyr Ile			
35	40	45	
Gly Thr Phe Gln Gly Ser Ser Phe Pro Asp Asn Asp Tyr Ala Trp Val			
50	55	60	
Ser Val Gly Ser Gly Trp Trp Thr Val Pro Val Val Leu Gly Trp Gly			
65	70	75	80
Thr Val Ser Asp Gln Leu Val Arg Gly Ser Asn Val Ala Pro Val Gly			
85	90	95	
Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr His Trp His Cys Gly Thr			
100	105	110	
Val Leu Ala His Asn Glu Thr Val Asn Tyr Ser Asp Gly Ser Val Val			
115	120	125	
His Gln Leu Thr Lys Thr Ser Val Cys Ala Glu Gly Gly Asp Ser Gly			
130	135	140	
Gly Ser Phe Ile Ser Gly Asp Gln Ala Gln Gly Val Thr Ser Gly Gly			
145	150	155	160
Trp Gly Asn Cys Ser Ser Gly Gly Glu Thr Trp Phe Gln Pro Val Asn			
165	170	175	
Glu Ile Leu Asn Arg Tyr Gly Leu Thr Leu His Thr Ala			
180	185		

<210> 43
<211> 197
<212> PRT
<213> Rarobacter faecitabidus

<400> 43

Val Ile Val Pro Val Arg Asp Tyr Trp Gly Gly Asp Ala Leu Ser Gly			
1	5	10	15
Cys Thr Leu Ala Phe Pro Val Tyr Gly Gly Phe Leu Thr Ala Gly His			
20	25	30	
Cys Ala Val Glu Gly Lys Gly His Ile Leu Lys Thr Glu Met Thr Gly			
35	40	45	

Gly Gln Ile Gly Thr Val Glu Ala Ser Gln Phe Gly Asp Gly Ile Asp
 50 55 60
 Ala Ala Trp Ala Lys Asn Tyr Gly Asp Trp Asn Gly Arg Gly Arg Val
 65 70 75 80
 Thr His Trp Asn Gly Gly Gly Val Asp Ile Lys Gly Ser Asn Glu
 85 90 95
 Ala Ala Val Gly Ala His Met Cys Lys Ser Gly Arg Thr Thr Lys Trp
 100 105 110
 Thr Cys Gly Tyr Leu Leu Arg Lys Asp Val Ser Val Asn Tyr Gly Asn
 115 120 125
 Gly His Ile Val Thr Leu Asn Glu Thr Ser Ala Cys Ala Leu Gly Gly
 130 135 140
 Asp Ser Gly Gly Ala Tyr Val Trp Asn Asp Gln Ala Gln Gly Ile Thr
 145 150 155 160
 Ser Gly Ser Asn Met Asp Thr Asn Asn Cys Arg Ser Phe Tyr Gln Pro
 165 170 175
 Val Asn Thr Val Leu Asn Lys Trp Lys Leu Ser Leu Val Thr Ser Thr
 180 185 190
 Asp Val Thr Thr Ser
 195

<210> 44
 <211> 191
 <212> PRT
 <213> Streptomyces coelicolor

<400> 44

Asp Pro Pro Leu Arg Ser Gly Leu Ala Ile Tyr Gly Thr Asn Val Arg
 1 5 10 15
 Cys Ser Ser Ala Phe Met Ala Tyr Ser Gly Ser Ser Tyr Tyr Met Met
 20 25 30
 Thr Ala Gly His Cys Ala Glu Asp Ser Ser Tyr Trp Glu Val Pro Thr
 35 40 45
 Tyr Ser Tyr Gly Tyr Gln Gly Val Gly His Val Ala Asp Tyr Thr Phe
 50 55 60
 Gly Tyr Tyr Gly Asp Ser Ala Ile Val Arg Val Asp Asp Pro Gly Phe
 65 70 75 80
 Trp Gln Pro Arg Gly Trp Val Tyr Pro Ser Thr Arg Ile Thr Asn Trp
 85 90 95
 Asp Tyr Asp Tyr Val Gly Gln Tyr Val Cys Lys Gln Gly Ser Thr Thr
 100 105 110
 Gly Tyr Thr Cys Gly Gln Ile Thr Glu Thr Asn Ala Thr Val Ser Tyr
 115 120 125
 Pro Gly Arg Thr Leu Thr Gly Met Thr Trp Ser Thr Ala Cys Asp Ala
 130 135 140
 Pro Gly Asp Ser Gly Ser Gly Val Tyr Asp Gly Ser Thr Ala His Gly
 145 150 155 160
 Ile Leu Ser Gly Gly Pro Asn Ser Gly Cys Gly Met Ile His Glu Pro
 165 170 175
 Ile Ser Arg Ala Leu Ala Asp Arg Gly Val Thr Leu Leu Ala Gly
 180 185 190

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
<223> primer

<400> 45
tgcgccgagc ccggcgactc 20

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 46
gagtcgcccgg gctcggcgca 20

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 47
ttcccccggca acgactacgc gtgggt 26

<210> 48
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 48
acccacgcgt agtcgttgcc gggaa 26

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 49
gccgctgctc gatcgggttc 20

<210> 50
<211> 24

<212> DNA
<213> Artificial Sequence

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<220>
<223> primer

<400> 50
gcagttgccg gagccgccc acgt 24

<210> 51
<211> 14
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<400> 51
tsggsgncrt ggtt 14

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 52

Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
1 5 10

<210> 53
<211> 555
<212> DNA
<213> Cellulomonas flavigena

<400> 53
gtcgacgtca tcggggcaa cgctactac atcgggtcgc gctcgccgtg ctgcgtcg 60
ttcgcggtcg agggcggtt cgtcaccgcg gggcactgcg ggcgcgcggg cgcgacacg 120
tcgtcaccgt cggggacatt ccgcggctcg tcgtccccg gcaacgacta cgcgtgggtc 180
caggtcgcct cgggcaacac gccgcgcggg ctggtaaca accactcggtt cggcacggtg 240
cgcgtcaccg gctcgcagca ggccgcggtc ggctcgatc tggccgatc gggcagcacg 300
acggatggc ggtgcggcta cgtccggcg tacaacacga ccgtgcggta cgcggagggc 360
tcggtctcg  gcctcatccg cacgagcgtg tgcggcggac cgggcgactc cggcggctcg 420
ctggtcgccc gcacgcaggc ccagggcgatc acgtcgccgcg ggtccggcaa ctgcgcgtac 480
ggggcacga cgtacttcca gcccgtaac gagatcctgc aggaccagcc cgggcccgtcg 540
accacgcgtg cccta 555

<210> 54
<211> 185

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<212> PRT
<213> Cellulomonas flavigena

<400> 54

Val Asp Val Ile Gly Gly Asn Ala Tyr Tyr Ile Gly Ser Arg Ser Arg
1 5 10 15
Cys Ser Ile Gly Phe Ala Val Glu Gly Gly Phe Val Thr Ala Gly His
20 25 30
Cys Gly Arg Ala Gly Ala Ser Thr Ser Ser Pro Ser Gly Thr Phe Arg
35 40 45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Ala Ser
50 55 60
Gly Asn Thr Pro Arg Gly Leu Val Asn Asn His Ser Gly Gly Thr Val
65 70 75 80
Arg Val Thr Gly Ser Gln Gln Ala Ala Val Gly Ser Tyr Val Cys Arg
85 90 95
Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Tyr Val Arg Ala Tyr Asn
100 105 110
Thr Thr Val Arg Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile Arg Thr
115 120 125
Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val Ala Gly
130 135 140
Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Tyr
145 150 155 160
Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln Asp Gln
165 170 175
Pro Gly Pro Ser Thr Thr Arg Ala Leu
180 185

<210> 55
<211> 1009
<212> DNA
<213> Cellulomonas biazotea

<400> 55

taaaaacagac ggccagtgaa tttgtataatc gactcaactat aggccaattt aatttagcg 60
ccgcgaattc gcccattaccc atagggcacg cgtggtcgac gcccctggcc tggtacgtcg 120
acgtcaactac caacacgtc gtgtcaacg ccaccgcct cggcgtggcc caggcgaccg 180
agatcgtcgc cgccgcaacg gtccccggcc acgcccgtccg ggtcgctcgag accaccgagg 240
cgccccgcac gttcatcgac gtcatcgccg gcaaccgtta ccggatcaac aacacctcgc 300
gctgctcggt cggttcgccc gtcagcggcg gcttcgtcac cggcgggcac tgcggcacga 360
ccggcgcgac cacgacgaaa ccgtccggca cggtccggg ctcgtcggtt cccggcaacg 420
actacgcgtg ggtgcgcgtc gcgtccggca acaccccggt cggcgcgttg aacaactaca 480
gcggcggcac cgtggccgtc gcccgtcga cgcaggcgac cgtcggtgcg tccgtctgcc 540
gctccggctc caccacgggg tggcgctgcg ggacgatcca ggcgttcaac tccaccgtca 600
actacgcgcga gggcagcgta tccggcctca tccgcacgaa cgtgtgcgc gagccggcg 660
actccggccg ctcgctcatc gccggcaacc agggccaggg cctgacgtcc ggcgggtcg 720
gcaactgcac caccggcgaa acgacgtact tccagccgt caacgaggcg ctctccgcct 780
acggcctgac gtcgtcaacg tcgtccggcg gggcggtgg cggcggcaccg acctgcaccg 840
ggtafcgcgcg gacctacacc ggctcgctcg cctcgccgca gtccggccgtc cagccgtccg 900
gcagctatgt gaccgtcggg tccagcggca ccatccgcgt ctgcctcgac ggcccggcg 960
ggacggactt cgacctgtac ctgcagaagt ggaacgggtc cgcgtggc 1009

<210> 56
<211> 335
<212> PRT

<213> Cellulomonas biazotea

<400> 56

Lys Gln Thr Ala Ser Glu Phe Val Ile Arg Leu Thr Ile Gly Glu Leu
1 5 10 15
Asn Leu Ala Ala Ala Asn Ser Pro Leu Pro Ile Gly His Ala Trp Ser
20 25 30
Thr Ala Leu Gly Trp Tyr Val Asp Val Thr Thr Asn Thr Val Val Val
35 40 45
Asn Ala Thr Ala Leu Ala Val Ala Gln Ala Thr Glu Ile Val Ala Ala
50 55 60
Ala Thr Val Pro Ala Asp Ala Val Arg Val Val Glu Thr Thr Glu Ala
65 70 75 80
Pro Arg Thr Phe Ile Asp Val Ile Gly Gly Asn Arg Tyr Arg Ile Asn
85 90 95
Asn Thr Ser Arg Cys Ser Val Gly Phe Ala Val Ser Gly Gly Phe Val
100 105 110
Thr Ala Gly His Cys Gly Thr Thr Gly Ala Thr Thr Thr Lys Pro Ser
115 120 125
Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val
130 135 140
Arg Val Ala Ser Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser
145 150 155 160
Gly Gly Thr Val Ala Val Ala Gly Ser Thr Gln Ala Thr Val Gly Ala
165 170 175
Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile
180 185 190
Gln Ala Phe Asn Ser Thr Val Asn Tyr Ala Gln Gly Ser Val Ser Gly
195 200 205
Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser
210 215 220
Leu Ile Ala Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly
225 230 235 240
Asn Cys Thr Thr Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala
245 250 255
Leu Ser Ala Tyr Gly Leu Thr Leu Val Thr Ser Ser Gly Gly Gly
260 265 270
Gly Gly Gly Thr Thr Cys Thr Gly Tyr Ala Arg Thr Tyr Thr Gly Ser
275 280 285
Leu Ala Ser Arg Gln Ser Ala Val Gln Pro Ser Gly Ser Tyr Val Thr
.290 295 300
Val Gly Ser Ser Gly Thr Ile Arg Val Cys Leu Asp Gly Pro Ser Gly
305 310 315 320
Thr Asp Phe Asp Leu Tyr Leu Gln Lys Trp Asn Gly Ser Ala Trp
325 330 335

<210> 57

<211> 474

<212> DNA

<213> Cellulomonas fimi

<400> 57

gtggacgtga tcggcgccga cgctactac atcggcgcc gcagccgctg ttgcgtatcg 60
ttcgccgtca ccgggggtt cgtgaccgccc gggcactgcg gccgcaccgg cgccggccacg 120
acgagccccgt cgggcacgtt cgccggctcg agcttccccgg gcaacgacta cgcgtgggtg 180
cgggtcgct cgggcaaacac gcccgtcgcc gcggtgaaca actacagcgg cggcacggtc 240

gccgtcgccg	gctcgaccca	ggccgcccgtc	ggtgcgaccg	tgtgccgctc	gggctccacc	300
accggctggc	ggtgccggcac	catccaggcg	ttcaacgcga	ccgtcaacta	cgccgagggc	360
agcgtctccg	gcctcatccg	cacgaacgtg	tgcgccgagc	coggcgactc	gggcggctcg	420
ctcgccg	gcaaccaggc	gcagggcatg	acgtccggcg	gctccgacaa	ctgc	474

<210> 58
<211> 144
<212> PRT
<213> Cellulomonas fimi

<400> 58

Val	Asp	Val	Ile	Gly	Gly	Asp	Ala	Tyr	Tyr	Ile	Gly	Gly	Arg	Ser	Arg
1															
														15	
Cys	Ser	Ile	Gly	Phe	Ala	Val	Thr	Gly	Gly	Phe	Val	Thr	Ala	Gly	His
														30	
Cys	Gly	Arg	Thr	Gly	Ala	Ala	Thr	Thr	Ser	Pro	Ser	Gly	Thr	Phe	Ala
														45	
Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Arg	Val	Ala	Ser
														60	
Gly	Asn	Thr	Pro	Val	Gly	Ala	Val	Asn	Asn	Tyr	Ser	Gly	Gly	Thr	Val
														80	
Ala	Val	Ala	Gly	Ser	Thr	Gln	Ala	Ala	Val	Gly	Ala	Thr	Val	Cys	Arg
														95	
Ser	Gly	Ser	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Thr	Ile	Gln	Ala	Phe	Asn
														110	
Ala	Thr	Val	Asn	Tyr	Ala	Glu	Gly	Ser	Val	Ser	Gly	Leu	Ile	Arg	Thr
														125	
Asn	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Val	Ala	Gly
														140	

<210> 59
<211> 462
<212> DNA
<213> Cellulomonas gelida

<400> 59

ctcgccggca	accaggcgca	gggcgtgacg	tccggcggt	cgggcaactg	ctcgccggc	60
gggacgacgt	acttccagcc	cgtcaaçgag	gccctccggg	tgtacgggt	cacgctcg	120
acctctgacg	gtgggggcac	cgagccgccc	ccgaccgggt	gccagggtct	tgcgcggacc	180
taccaggcgca	gcgtctcg	cgggacgtcg	gtcgccgac	cgaacgggttc	gtacgtcacg	240
accggggcg	ggacgcaccc	ggtgtgcctg	agcggacccgg	cgggcacgg	cctggacctg	300
tacctgcaga	agtggAACCG	gtactcg	gccagcg	cgcagtcgac	gtcgctgg	360
gccacggagg	cggta	caccgggacc	gccggctact	accgctacgt	ggtccacg	420
tacgcgggtt	cggggcgta	caccctgggg	gacgacccc	cg		462

<210> 60
<211> 154
<212> PRT
<213> Cellulomonas gelida

<400> 60

Leu	Ala	Gly	Asn	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Ser	Gly	Asn	
1															
														15	
Cys	Ser	Ser	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val	Asn	Glu	Ala	Leu
														30	
Arg	Val	Tyr	Gly	Leu	Thr	Leu	Val	Thr	Ser	Asp	Gly	Gly	Thr	Glu	

35	40	45
Pro Pro Pro Thr Gly Cys Gln Gly Tyr Ala Arg Thr Tyr Gln Gly Ser		
50	55	60
Val Ser Ala Gly Thr Ser Val Ala Gln Pro Asn Gly Ser Tyr Val Thr		
65	70	75
Thr Gly Gly Thr His Arg Val Cys Leu Ser Gly Pro Ala Gly Thr		
85	90	95
Asp Leu Asp Leu Tyr Leu Gln Lys Trp Asn Gly Tyr Ser Trp Ala Ser		
100	105	110
Val Ala Gln Ser Thr Ser Pro Gly Ala Thr Glu Ala Val Thr Tyr Thr		
115	120	125
Gly Thr Ala Gly Tyr Tyr Arg Tyr Val Val His Ala Tyr Ala Gly Ser		
130	135	140
Gly Ala Tyr Thr Leu Gly Ala Thr Thr Pro		
145	150	

<210> 61

<211> 257

<212> DNA

<213> Cellulomonas iranensis

<400> 61

ttccccggca acgactacgc gtgggtccag gtcgggtcgg gcgacacccc ccgcggcctg	60
gtcaacaact acgcgggcgg caccgtcgg gtcacccgggt cgacggcaggc cgccgtcggc	120
gcgtacgtct gccgggtcggg cagcacgacg ggctggcgct gccggcaccgt gcaggcctac	180
aacgcgtcgg tccgctacgc cgagggcacc gtctcgggcc tcatccgcac caacgtctgc	240
gccgagcccg gcgactc	257

<210> 62

<211> 85

<212> PRT

<213> Cellulomonas iranensis

<400> 62

Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Gly Ser Gly Asp Thr		
1 5 10 15		
Pro Arg Gly Leu Val Asn Asn Tyr Ala Gly Gly Thr Val Arg Val Thr		
20 25 30		
Gly Ser Gln Gln Ala Ala Val Gly Ala Tyr Val Cys Arg Ser Gly Ser		
35 40 45		
Thr Thr Gly Trp Arg Cys Gly Thr Val Gln Ala Tyr Asn Ala Ser Val		
50 55 60		
Arg Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys		
65 70 75 80		
Ala Glu Pro Gly Asp		
85		

<210> 63

<211> 904

<212> DNA

<213> Cellulomonas cellasea

<400> 63

gtcgggcggg tccggcaact gccgctacgg gggcacgacg tacttccagc ccgtgaacga	60
gatcctgcag gcctacggtc tgcgtctcggt cctgggctga cacgctcgcg gcggggccgg	120
ctcgacgcgg ccggcccggtc ggcccggtc gcccgcgtt acgtcgacgt gcccaccaac	180

aagctcgtcg	tcgagtccgt	cggcgacacc	gccccggccg	ccgacgcgt	cgccgccgcg	240
ggcctgcctg	ccgacgcgt	gacgctcgt	accacccagg	cgccacggac	gttcgtcgac	300
gtcatcggcg	gcaacgcgt	ctacatcaac	gcgagcagcc	gctgctcggt	cggcttcgcg	360
gtcgagggcg	ggttcgctac	cgcgggcccac	tgcgggcccgc	cgggcgcgag	cacgtcgtca	420
ccgctgggga	ccttccggcg	ctcgctgttc	cccggcaacg	actacgcgtg	ggtccaggtc	480
gcctcggca	acacgcgcg	cgggctggtg	aacaaccact	cgggcggcac	ggtgcgcgtc	540
accggctcgc	agcaggccgc	ggtcggctcg	tacgtgtgcc	gatcgggcag	cacgacggga	600
tggcggcgc	gctacgtccg	ggcgtacaac	acgaccgtgc	ggtacgcgga	gggctcggtc	660
tcggcgccta	tccgcacgag	cgtgtgcgc	gagccggcgg	actccggcgg	ctcgctggtc	720
gccggcacgc	aggcccagg	cgtcacgtcg	ggcgggtccg	gcaactgccc	ctacgggggc	780
acgacgtact	tccagccgt	gaacgagatc	ctgcaggcct	acggtctgcg	tctcgctctg	840
ggctgacacg	ctcgccggcg	gccctcccct	gcccgtcgcg	cggccggcccc	accagcccg	900
						904

<210> 64
<211> 300
<212> PRT
<213> Cellulomonas cellasea

<400> 64

Val	Gly	Arg	Val	Arg	Gln	Leu	Pro	Leu	Arg	Gly	His	Asp	Val	Leu	Pro
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Ala	Arg	Glu	Arg	Asp	Pro	Ala	Gly	Leu	Arg	Ser	Ala	Ser	Arg	Pro	Gly
								20		25				30	
Leu	Thr	Arg	Ser	Arg	Arg	Ala	Arg	Leu	Asp	Ala	Ala	Gly	Pro	Ser	Ala
								35		40				45	
Arg	Val	Ala	Ala	Trp	Tyr	Val	Asp	Val	Pro	Thr	Asn	Lys	Leu	Val	Val
						50		55			60				
Glu	Ser	Val	Gly	Asp	Thr	Ala	Ala	Ala	Asp	Ala	Val	Ala	Ala	Ala	
						65		70		75				80	
Gly	Leu	Pro	Ala	Asp	Ala	Val	Thr	Leu	Ala	Thr	Thr	Glu	Ala	Pro	Arg
						85			90			95			
Thr	Phe	Val	Asp	Val	Ile	Gly	Gly	Asn	Ala	Tyr	Tyr	Ile	Asn	Ala	Ser
						100		105			110				
Ser	Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Glu	Gly	Gly	Phe	Val	Thr	Ala
						115		120			125				
Gly	His	Cys	Gly	Arg	Ala	Gly	Ala	Ser	Thr	Ser	Ser	Pro	Ser	Gly	Thr
						130		135			140				
Phe	Arg	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Gln	Val
						145		150		155				160	
Ala	Ser	Gly	Asn	Thr	Pro	Arg	Gly	Leu	Val	Asn	Asn	His	Ser	Gly	Gly
						165			170				175		
Thr	Val	Arg	Val	Thr	Gly	Ser	Gln	Gln	Ala	Ala	Val	Gly	Ser	Tyr	Val
						180			185			190			
Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Tyr	Val	Arg	Ala
						195		200			205				
Tyr	Asn	Thr	Thr	Val	Arg	Tyr	Ala	Glu	Gly	Ser	Val	Ser	Gly	Leu	Ile
						210		215			220				
Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Val
						225		230		235				240	
Ala	Gly	Thr	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys
						245			250			255			
Arg	Tyr	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val	Asn	Glu	Ile	Leu	Gln
						260			265			270			
Ala	Tyr	Gly	Leu	Arg	Leu	Val	Leu	Gly	His	Ala	Arg	Gly	Gly	Pro	Ser
						275			280			285			

Pro Ala Arg Arg Ala Pro Ala Pro Pro Ala Arg Ala
290 295 300

<210> 65
<211> 429
<212> DNA
<213> Cellulomonas xylinolytica

<400> 65
cgctgctcga tcgggttcgc cgtgacgggc ggcttcgtga ccgcccggcca ctgcggacgg 60
tccggcgcga cgacgacgtc gccgagcggc acgttcggcg gttccagctt tccccggcaac 120
gactacgcct gggtccgcgc ggcctcgggc aacacgcccgg tcggtgccggt gaaccgctac 180
gacggcagcc gggtgaccgt ggcgggttcc accgacgcgg ccgtcggtgc cgccgtctgc 240
cggtcgggggt cgacgaccgc gtggggctgc ggcacgatcc agtccccgggg cgcgagcgtc 300
acgtacgccc agggcaccgt cagcgggctc atccgcacca acgtgtgcgc cgagccgggt 360
gactccgggg ggtcgctgat cgccggcacc caggcggggg gcgtgacgta cgccggctcc 420
ggcaactgc 429

<210> 66
<211> 143
<212> PRT
<213> Cellulomonas xylinolytica

<400> 66

Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly
1 5 10 15
His Cys Gly Arg Ser Gly Ala Thr Thr Thr Ser Pro Ser Gly Thr Phe
20 25 30
Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala
35 40 45
Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg
50 55 60
Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys
65 70 75 80
Arg Ser Gly Ser Thr Thr Ala Trp Gly Cys Gly Thr Ile Gln Ser Arg
85 90 95
Gly Ala Ser Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg
100 105 110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala
115 120 125
Gly Thr Gln Ala Arg Gly Val Thr Ser Gly Gly Ser Gly Asn Cys
130 135 140

<210> 67
<211> 1284
<212> DNA
<213> Oerskovia turbata

<400> 67
atggcacat cattctggag gacgctcgcc acggcggtcgcc ccgcgcacggc actgggtgcc 60
ggcccccgcag cgctcaccgc gaacgcccggc acgcccaccc ccgcacacccc gaccgtttca 120
ccccagaccc cctcgaaggt ctgcggcgag gtgctccgcg ccctccagcg ggacctgggg 180
ctgagcgcca aggacgcgac gaagcgctcg gcgttccagt ccgcacgcggc gagcaccgag 240
gacgcctctcg ccgcacagcc ggacgcctac gcggggccct gggtcgaccc tgcgaggaac 300
accctgtacg tcggcgctcg ccacaggccc gaggccaagg aggtccgttc ggccggagcg 360
accggcgatgg tcgtcgacca caccgtcgcc gagctcgaca cgtggaaaggc ggccgtcgac 420

ggtagagctca	acgacccccgc	gggcgtcccg	agctggttcg	tcgacgtcac	gaccaaccag	480
gtcgtcgta	acgtgcacga	cggcggacgc	gccctcgccg	agctggctgc	cgcgagcgcg	540
ggcgtgcccgc	ccgacgcatt	cacctacgtg	acgacgaccg	aggctcctcg	tcccctcg	600
gacgtggtgg	gcccccaacgc	gtacaccatg	ggttcggg	ggcgctgctc	ggtcggcttc	660
gccccgtaaac	ggggcttcat	cacggccggg	cactgcggct	cggtcggcac	ccgcacac	720
gggcggggcg	gcacgttccg	ggggtcgaac	ttccccggca	acgactacgc	ctgggtgcag	780
gtcgtcgccg	gtaaacacccc	ggtcggcg	gtcaacaact	acagcggtg	gccccgtcg	840
gtcgcagggt	cgacggccgc	gcccgtgggg	gcctcggtct	gccggccgg	ttccacgac	900
ggctggcact	gccccgtacat	cggcgtac	aacaccc	tgacgtaccc	gcagggcacc	960
gtctggggc	tcatccgcac	gaacgtgtgc	gccgagccc	gcgactcg	cggctcg	1020
ctcgccggca	accaggcgca	ggcggtgacc	tcggccgggt	cggcaactg	ctcgccggc	1080
gggacgacgt	acttccagcc	cgtcaacgag	gccctcg	ggtacggct	cacgcgtcg	1140
acctctgacg	gtggggggcc	gagccgccc	cgaccgggt	ccagggtat	gccccgtcg	1200
accagggcag	cgtctcgcc	gggacgtcg	tcgcccagc	aacgggtcg	acgtcacgac	1260
cggggccggg	cgaccgggt	tgcc				1284

<210> 68

<211> 428

<212> PRT

<213> Oerskovia turbata

<400> 68

Met	Ala	Arg	Ser	Phe	Trp	Arg	Thr	Leu	Ala	Thr	Ala	Cys	Ala	Ala	Thr
1				5				10				15			
Ala	Leu	Val	Ala	Gly	Pro	Ala	Ala	Leu	Thr	Ala	Asn	Ala	Ala	Thr	Pro
					20				25			30			
Thr	Pro	Asp	Thr	Pro	Thr	Val	Ser	Pro	Gln	Thr	Ser	Ser	Lys	Val	Ser
						35			40			45			
Pro	Glu	Val	Leu	Arg	Ala	Leu	Gln	Arg	Asp	Leu	Gly	Leu	Ser	Ala	Lys
					50			55			60				
Asp	Ala	Thr	Lys	Arg	Leu	Ala	Phe	Gln	Ser	Asp	Ala	Ala	Ser	Thr	Glu
					65			70			75			80	
Asp	Ala	Leu	Ala	Asp	Ser	Leu	Asp	Ala	Tyr	Ala	Gly	Ala	Trp	Val	Asp
					85			90			95				
Pro	Ala	Arg	Asn	Thr	Leu	Tyr	Val	Gly	Val	Ala	Asp	Arg	Ala	Glu	Ala
					100			105			110				
Lys	Glu	Val	Arg	Ser	Ala	Gly	Ala	Thr	Pro	Val	Val	Asp	His	Thr	
					115			120			125				
Leu	Ala	Glu	Leu	Asp	Thr	Trp	Lys	Ala	Ala	Leu	Asp	Gly	Glu	Leu	Asn
					130			135			140				
Asp	Pro	Ala	Gly	Val	Pro	Ser	Trp	Phe	Val	Asp	Val	Thr	Thr	Asn	Gln
					145			150			155			160	
Val	Val	Val	Asn	Val	His	Asp	Gly	Gly	Arg	Ala	Leu	Ala	Glu	Leu	Ala
					165			170			175				
Ala	Ala	Ser	Ala	Gly	Val	Pro	Ala	Asp	Ala	Ile	Thr	Tyr	Val	Thr	Thr
					180			185			190				
Thr	Glu	Ala	Pro	Arg	Pro	Leu	Val	Asp	Val	Val	Gly	Gly	Asn	Ala	Tyr
					195			200			205				
Thr	Met	Gly	Ser	Gly	Gly	Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Asn	Gly
					210			215			220				
Gly	Phe	Ile	Thr	Ala	Gly	His	Cys	Gly	Ser	Val	Gly	Thr	Arg	Thr	Ser
					225			230			235			240	
Gly	Pro	Gly	Gly	Thr	Phe	Arg	Gly	Ser	Asn	Phe	Pro	Gly	Asn	Asp	Tyr
					245			250			255				
Ala	Trp	Val	Gln	Val	Asp	Ala	Gly	Asn	Thr	Pro	Val	Gly	Ala	Val	Asn
					260			265			270				

Asn Tyr Ser Gly Gly Arg Val Ala Val Ala Gly Ser Thr Ala Ala Pro
 275 280 285
 Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys
 290 295 300
 Gly Thr Ile Gly Ala Tyr Asn Thr Ser Val Thr Tyr Pro Gln Gly Thr
 305 310 315 320
 Val Ser Gly Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser
 325 330 335
 Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly
 340 345 350
 Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val
 355 360 365
 Asn Glu Ala Leu Gly Gly Tyr Gly Leu Thr Leu Val Thr Ser Asp Gly
 370 375 380
 Gly Gly Pro Ser Arg Arg Arg Pro Gly Ala Arg Ala Met Arg Gly Pro
 385 390 395 400
 Thr Arg Ala Ala Ser Arg Pro Gly Arg Arg Ser Arg Ser Glu Arg Phe
 405 410 415
 Val Arg His Asp Arg Gly Arg Ala Thr Gly Cys Ala
 420 425

<210> 69
 <211> 524
 <212> DNA
 <213> Oerskovia jenensis

<400> 69
 gcccgtgctc ggtcggcttc gcgggtgaacg gcggcttcgt caccgcaggc cactgcggga 60
 cggtgggcac ccgcaccccg gggccggcg gcacgttccg cgggtcgagc ttccccggca 120
 acgactacgc ctgggtgcag gtgcacgcgg ggaacacccc ggtcggggcc gtcaacaact 180
 acagcggtgg acgcgtcgcg gtgcgggct cgacggccgc acccgtgggt tcctcggtct 240
 gccggccgg ttccacgacg ggctggcgct gcggcacgat cgccgcctac aacagctcg 300
 tgacgtaccc gcaggggacc gtctccggc tcatccgcac caacgtgtgc gccgagccgg 360
 gcgactcggg cggctcgctc ctgcgggca accaggcaca gggcctgacg tcggccgggt 420
 cggcaactg ctgcgtggc ggcacgacgt acttccagcc cgtcaacgag gcgctctcg 480
 cttacggcct cacgctcggt acctccggcg gcagggcaa ctgc 524

<210> 70
 <211> 174
 <212> PRT
 <213> Oerskovia jenensis

<400> 70

Arg Cys Ser Val Gly Phe Ala Val Asn Gly Gly Phe Val Thr Ala Gly
 1 5 10 15
 His Cys Gly Thr Val Gly Thr Arg Thr Ser Gly Pro Gly Gly Thr Phe
 20 25 30
 Arg Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Asp
 35 40 45
 Ala Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Arg
 50 55 60
 Val Ala Val Ala Gly Ser Thr Ala Ala Pro Val Gly Ser Ser Val Cys
 65 70 75 80
 Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile Ala Ala Tyr
 85 90 95
 Asn Ser Ser Val Thr Tyr Pro Gln Gly Thr Val Ser Gly Leu Ile Arg

100 105 110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala

115 120 125
Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Ser
130 135 140
Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala Leu Ser Ala
145 150 155 160
Tyr Gly Leu Thr Leu Val Thr Ser Gly Gly Arg Gly Asn Cys
165 170

<210> 71

<211> 984

<212> DNA

<213> Cellulosimicrobium cellulans

<400> 71

ccacgggcgg cgggtcgggc agcgcgctcg tcgggctcgc gggcaagtgc atcgacgtcc 60
ccgggtccga cttagtgcac ggaaagcgcc tccagctgtg gacgtgcaac gggtcgcagg 120
cagcgctgga cgttcgaagc cgacggcacc gtacgcgcgg gcggcaagtgc catggacgtc 180
gcgtggcgcgc cgccggccgac ggacacggcgc tccagctcgc gaactgcacg gcaacgcggc 240
ccagaagttc gtgctcaacg gcgcggcga cctcgtgtcg gtgctggcga acaaagtgcg 300
tcgacgcgcgc cgggtgcgca ccgaggtact cgccggcgcg tacgagctea cggcgacgtg 360
cgccggcggcgc accgctacat cacacgggac ccggggcgcgt cgtcgggctc ggcctgctcg 420
atcgggtacg ccttccaggg cggcttcgtc acggcggggc actgcggacg cggcgggaca 480
aggagagtgcc tcaccgcgag ctgggcgcgc atggggacgg tccaggcggc gtcgcccc 540
ggccacgact acgcgtgggt gcgcgtcgac gccgggtct ccccggtccc gcgggtgaac 600
aactacgccc gccggcaccgt cgacgtcgcc ggctcggccg aggcccccgt ggggtgcgtcg 660
gtgtgcgcgt cgggcgcac gaccggctgg cgctgcggcg tcatcgagca gaagaacatc 720
accgtcaact acggcaacgg cgacgttccc ggcctcgtgc gccggcagcgc gtgcgcggag 780
ggcggcgaact cgggcggggtc ggtatctcc ggcaaccagg cgcaggcgt cacgtcgggc 840
aggatcaacg actgctcgaa cggcggcaag ttctctacc agcccgtcg acggcctgtc 900
gctcgtgacc acggcggcgc ggtcggcag cgctcgtc gggctcgcgg gcaagtgcac 960
cgacgtcccc gggtccgact tcag 984

<210> 72

<211> 328

<212> PRT

<213> Cellulosimicrobium cellulans

<400> 72

Pro Arg Ala Ala Gly Arg Ala Ala Arg Ser Ser Gly Ser Arg Ala Ser
1 5 10 15
Ala Ser Thr Ser Pro Gly Pro Thr Ser Val Thr Ala Ser Ala Ser Ser
20 25 30
Cys Gly Arg Ala Thr Gly Arg Arg Gln Arg Trp Thr Phe Glu Ala Asp
35 40 45
Gly Thr Val Arg Ala Gly Gly Lys Cys Met Asp Val Ala Trp Ala Pro
50 55 60
Arg Pro Thr Ala Arg Arg Ser Ser Ser Arg Thr Ala Arg Gln Arg Gly
65 70 75 80
Pro Glu Val Arg Ala Gln Arg Arg Gly Arg Pro Arg Val Gly Ala Gly
85 90 95
Glu Gln Ser Ala Ser Thr Pro Pro Gly Ala His Arg Gly Thr Arg Gly

	100	105	110
Ala Val Arg Ala His Gly Asp Val Arg Gly Gly Asp Arg Tyr Ile Thr			
115	120	125	
Arg Asp Pro Gly Ala Ser Ser Gly Ser Ala Cys Ser Ile Gly Tyr Ala			
130	135	140	
Val Gln Gly Gly Phe Val Thr Ala Gly His Cys Gly Arg Gly Gly Thr			
145	150	155	160
Arg Arg Val Leu Thr Ala Ser Trp Ala Arg Met Gly Thr Val Gln Ala			
165	170	175	
Ala Ser Phe Pro Gly His Asp Tyr Ala Trp Val Arg Val Asp Ala Gly			
180	185	190	
Phe Ser Pro Val Pro Arg Val Asn Asn Tyr Ala Gly Gly Thr Val Asp			
195	200	205	
Val Ala Gly Ser Ala Glu Ala Pro Val Gly Ala Ser Val Cys Arg Ser			
210	215	220	
Gly Ala Thr Thr Gly Trp Arg Cys Gly Val Ile Glu Gln Lys Asn Ile			
225	230	235	240
Thr Val Asn Tyr Gly Asn Gly Asp Val Pro Gly Leu Val Arg Gly Ser			
245	250	255	
Ala Cys Ala Glu Gly Gly Asp Ser Gly Gly Ser Val Ile Ser Gly Asn			
260	265	270	
Gln Ala Gln Gly Val Thr Ser Gly Arg Ile Asn Asp Cys Ser Asn Gly			
275	280	285	
Gly Lys Phe Leu Tyr Gln Pro Asp Arg Arg Pro Val Ala Arg Asp His			
290	295	300	
Gly Arg Arg Val Gly Gln Arg Ala Arg Arg Ala Arg Gly Gln Val His			
305	310	315	320
Arg Arg Pro Arg Val Arg Leu Gln			
	325		

<210> 73
<211> 257
<212> DNA
<213> Promicromonospora citrea

<400> 73
ttccccggca acgactacgc gtgggtgaac acgggcacgg acgacaccct cgtcgccgcc 60
gtgaacaact acagcggcgg cacggtaaac gtcgcgggct cgaccgtgc cgccgtcggc 120
gcaacggctt gcccgtcggg ctccacgacc ggctggact gcggcaccat ccaggcgctg 180
aacgcgtcgg tcacctacgc cgagggcacc gtgagcggcc tcatccgcac caacgtgtgc 240
gccgagcccg gcgactc 257

<210> 74
<211> 85
<212> PRT
<213> Promicromonospora citrea

<400> 74

Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Thr Gly Thr Asp Asp Thr			
1	5	10	15
Leu Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala			
20	25	30	
Gly Ser Thr Arg Ala Ala Val Gly Ala Thr Val Cys Arg Ser Gly Ser			
35	40	45	
Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Leu Asn Ala Ser Val			
50	55	60	

Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65 70 75 80
Ala Glu Pro Gly Asp
85

<210> 75
<211> 257
<212> DNA
<213> Promicromonospora sukumoe

<400> 75
ttccccggca acgactacgc gtgggtgaac gtcggctccg acgacacccc gatcggtgcg 60
gtcaacaact acagcggcgg caccgtgaac gtcgcggct cgacccaggc cgccgtcggc 120
tccaccgtct gccgctccgg ttccacgacc ggctggact gcggcaccat ccaggccttc 180
aacgcgtcgg tcacctacgc cgagggcacc gtgtccggcc tgcgtccgcac caacgtctgc 240
gccgagcccg gcgactc 257

<210> 76
<211> 85
<212> PRT
<213> Promicromonospora sukumoe

<400> 76

Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Val Gly Ser Asp Asp Thr
1 5 10 15
Pro Ile Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala
20 25 30
Gly Ser Thr Gln Ala Ala Val Gly Ser Thr Val Cys Arg Ser Gly Ser
35 40 45
Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Phe Asn Ala Ser Val
50 55 60
Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65 70 75 80
Ala Glu Pro Gly Asp
85

<210> 77
<211> 430
<212> DNA
<213> Xylanibacterium ulmi

<400> 77
gccgctgctc gatcgggttc gccgtgacgg gcggcttcgt gaccgcggc cactgcggac 60
ggtcggcgc gacgacgacg tccgcgagcg gcacgttcgc cgggtccagc tttccggca 120
acgactacgc ctgggtccgc gcggcctcgg gaacacgccc gtcgggtcgg tgaacctcta 180
cgacggcagc cgggtgaccc tgccgggtc caccgacgcg gccgtcggtg ccgcgtctg 240
ccggtcgggg tcgacgaccc cgtggcgctg cggcacgatc cagtcccgcg gcgcgacggt 300
cacgtacgcc cagggcaccc tcagcggct catccgcacc aacgtgtcgc cggagccggg 360
tgactccggg gggtegctga tcgcgggcac ccaggcgcag ggcgtgacgt ccggcggctc 420
cggcaactgc 430

<210> 78
<211> 141
<212> PRT
<213> Xylanibacterium ulmi

<400> 78

Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly
1 5 10 15
His Cys Gly Arg Ser Gly Ala Thr Thr Ser Ala Ser Gly Thr Phe
20 25 30
Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala
35 40 45
Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg
50 55 60
Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys
65 70 75 80
Arg Ser Gly Ser Thr Thr Ala Trp Arg Cys Gly Thr Ile Gln Ser Arg
85 90 95
Gly Ala Thr Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg
100 105 110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala
115 120 125
Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly
130 135 140

<210> 79

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 79

acccacgcgt agtcgttgcc 20

<210> 80
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 80

acccacgcgt agtcgtkgcc gggg 24

<210> 81
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 81

tcgtcgtggc cgcccg 18

<210> 82
<211> 17

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 82		
cgacgtgctc gcggcccg		17
<210> 83		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 83		
cgcgcccagc tcgcggtg		18
<210> 84		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 84		
cggcccccagc gtgcgggtgc cg		22
<210> 85		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 85		
cagcgtctcc ggctcatcc gc		22
<210> 86		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 86		
ctcggtctcg ggctcatcc gc		22
<210> 87		
<211> 22		
<212> DNA		
<213> Artificial Sequence		

<220>
<223> primer

<400> 87
cgacgttccc ggcctcgtgc gc 22

<210> 88
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 88
caccgtctcg gggctcatcc gc 22

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 89
agcarcgtgt gcgccgagcc 20

<210> 90
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 90
ggcagcgcgt gcgcggaggg 20

<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 91
gccgctgctc gatcgggttc 20

<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

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<223> primer

<400> 92
gcagttgccg gagccgcccc acgt 24

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 93
tgcggcgagc ccggcgactc cggc 24

<210> 94
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 94
ggcacgacgt acttccagcc cgtgaac 27

<210> 95
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 95
gaccCACGCG tagtcgttgc cggggAACGA CGA 33

<210> 96
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 96
gaaggTCCCC GACGGTGACG ACGTGCTCGC GCC 33

<210> 97
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer
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<400> 97
caggcgcagg gcgtgacctc gggcggtcg 30

<210> 98
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 98
ggcgggacga cgtacttcca gcccgtaaa 29

<210> 99
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 99
cacccacgcg tagtcgtggc cggggAACGA 30

<210> 100
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 100
gaagccgccc tggacggcgt acccgatcga gca 33

<210> 101
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 101
tgcgcggagg gcggcgactc gggcggtcg 30

<210> 102
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 102
ttcctctacc agcccgtaaa cccgatccta 30

<210> 103
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 103
cgccgcgggg acgaaccgc cctcgaccgc gaa 33

<210> 104
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 104
cgcgtatcg ttgccgggaa acgacgagcc 30

<210> 105
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 105
ggcctcatcc gcacgagcgt gtgcgccgag 30

<210> 106
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 106
acgtcggcg ggtccggcaa ctgccgtac gggggc 36

<210> 107
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 107
gagcccgtag acccggaggg cctcggttgc gggctggaa 39

<210> 108
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 108
cgtcacgccc tgccgcctggc tgcccgcgag 30

<210> 109
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 109
tccagccccgt caacgaggcc ctccgggtgt acgggctc 38

<210> 110
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 110
acgttcggtcg cgcagccgaa cgggttcgtac gtc 33

<210> 111
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 111
cgtggtcgctg cccgggtcgatgc cgcaagtgcggcc 30

<210> 112
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 112
gacgacgacc gtgttgttag tgacgtcgac gtacca 36

<210> 113

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 113
tccaccacgg ggtggcgctg cgggacgatc 30

<210> 114
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 114
gtgtgcgcgg agccccggcga ctccggcggc 30

<210> 115
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 115
gctcgggccc ccaccgtcag aggtcacgag cgtgag 36

<210> 116
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 116
atggcacgat cattctggag gacgctcgcc acggcg 36

<210> 117
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 117
tgctcgatcg ggtacgcccgt ccagggcggc ttc 33

<210> 118
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 118
taggatcggg ttgacgggct ggttagaggaa 30

<210> 119

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 119
tggtagtcg acgtcaactac caacacggc gtcgtc 36

<210> 120

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 120
gccgcggag tcgccccggct cggcgcacac 30

<210> 121

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 121
gtsgacgtsa tcggsggsaa cgctactac 30

<210> 122

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (13)..(16)

<223> n is a, c, g, or t

<400> 122
sgcsgtsgcs ggnganga 18

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<210> 123
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 123
gtsgaygtsa tcggcggcga ygcstac 27

<210> 124
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (10)..(16)
<223> n is a, c, g, or t

<400> 124
sgasgcgtan ccctgncc 18

<210> 125
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> VARIANT
<222> 1, 8-16, 24, 35, 36, 38, 39, 41-44, 48, 61-64, 66, 67, 69-71, 81, 87, 89,
93, 109-111, 113, 116
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> 4, 19, 28, 108, 126
<223> Xaa is Ile or Val

<220>
<221> VARIANT
<222> 7, 157
<223> Xaa is Asn or Asp

<220>
<221> VARIANT
<222> 92, 99, 143
<223> Xaa is Ser or Ala
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<220>
<221> VARIANT
<222> 112, 156
<223> Xaa is Asn or Gly

<220>
<221> VARIANT
<222> 21
<223> Xaa is Phe or Tyr

<220>
<221> VARIANT
<222> 40
<223> Xaa is Thr or Val

<220>
<221> VARIANT
<222> 59
<223> Xaa is Phe or Trp

<220>
<221> VARIANT
<222> 65
<223> Xaa is Gly or Asp

<220>
<221> VARIANT
<222> 68
<223> Xaa is Leu or Phe

<220>
<221> VARIANT
<222> 74
<223> Xaa is Asn or Arg

<220>
<221> VARIANT
<222> 75
<223> Xaa is Tyr or His

<220>
<221> VARIANT
<222> 76
<223> Xaa is Ser or Asp

<220>
<221> VARIANT
<222> 78
<223> Xaa is Gly or Ser

<220>
<221> VARIANT
<222> 79
<223> Xaa is Arg or Thr

<220>
<221> VARIANT

<222> 83
<223> Xaa is Ala or Thr

<220>
<221> VARIANT
<222> 85
<223> Xaa is His or Ser

<220>
<221> VARIANT
<222> 86
<223> Xaa is Thr or Gln

<220>
<221> VARIANT
<222> 102
<223> Xaa is Gly or Ala

<220>
<221> VARIANT
<222> 104
<223> Xaa is His or Arg

<220>
<221> VARIANT
<222> 107
<223> Xaa is Thr or Tyr

<220>
<221> VARIANT
<222> 114
<223> Xaa is Ser or Thr

<220>
<221> VARIANT
<222> 118
<223> Xaa is Pro or Ala

<220>
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<222> 119
<223> Xaa is Glu or Gln

<220>
<221> VARIANT
<222> 121
<223> Xaa is Thr, Ser, or Asp

<220>
<221> VARIANT
<222> 123
<223> Xaa is Arg or Ser

<220>
<221> VARIANT
<222> 128
<223> Xaa is Thr or Gly

<220>
<221> VARIANT
<222> 129
<223> Xaa is Thr, Asn, or Ser

<220>
<221> VARIANT
<222> 130
<223> Xaa is Val or Ala

<220>
<221> VARIANT
<222> 134
<223> Xaa is Pro or Gly

<220>
<221> VARIANT
<222> 141
<223> Xaa is Leu or Val

<220>
<221> VARIANT
<222> 142
<223> Xaa is Leu, Val, or Ile

<220>
<221> VARIANT
<222> 145
<223> Xaa is Asn or Thr

<220>
<221> VARIANT
<222> 148
<223> Xaa is Gln or Arg

<220>
<221> VARIANT
<222> 150
<223> Xaa is Val or Leu

<220>
<221> VARIANT
<222> 154
<223> Xaa is Gly or Arg

<220>
<221> VARIANT
<222> 155
<223> Xaa is Ser or Ile

<220>
<221> VARIANT
<222> 159, 160, 163-166, 169-189
<223> Xaa can be any naturally occurring amino acid

<400> 125

Xaa Asp Val Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Cys Ser Xaa Gly Xaa Ala Val Xaa Gly Gly Phe Xaa Thr Ala Gly His
 20 25 30
 Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Gly Thr Phe Xaa
 35 40 45
 Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Xaa Val Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Val Asn Xaa Xaa Xaa Gly Xaa Xaa Val
 65 70 75 80
 Xaa Val Xaa Gly Xaa Xaa Xaa Ala Xaa Val Gly Xaa Xaa Val Cys Arg
 85 90 95
 Ser Gly Xaa Thr Thr Xaa Trp Xaa Cys Gly Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110
 Xaa Xaa Val Xaa Tyr Xaa Xaa Gly Xaa Val Xaa Gly Leu Xaa Arg Xaa
 115 120 125
 Xaa Xaa Cys Ala Glu Xaa Gly Asp Ser Gly Gly Ser Xaa Xaa Xaa Gly
 130 135 140
 Xaa Gln Ala Xaa Gly Xaa Thr Ser Gly Xaa Xaa Xaa Xaa Cys Xaa Xaa
 145 150 155 160
 Gly Gly Xaa Xaa Xaa Xaa Gln Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175
 Xaa
 180 185

<210> 126
 <211> 16
 <212> PRT
 <213> Cellulomonas cellasea

<220>
 <221> VARIANT
 <222> (1)..(1)
 <223> Xaa is Ile or Tyr

<400> 126

Xaa Ala Trp Asp Ala Phe Ala Glu Asn Val Val Asp Trp Ser Ser Arg
 1 5 10 15

<210> 127
 <211> 17
 <212> PRT
 <213> Cellulomonas cellasea

<400> 127

Tyr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln Ala
 1 5 10 15
 Tyr

<210> 128
 <211> 11
 <212> PRT
 <213> Cellulomonas flavigena

<220>
 <221> VARIANT
 <222> (4)..(11)
 <223> Xaa is Ile or Tyr

 <400> 128

Val Asp Val Xaa Gly Gly Asn Ala Tyr Tyr Xaa
 1 5 10

<210> 129
 <211> 9
 <212> PRT
 <213> Cellulomonas fimi

<220>
 <221> VARIANT
 <222> (4)..(4)
 <223> Xaa is Ile or Tyr

 <400> 129

Val Asp Val Xaa Gly Gly Asp Ala Tyr
 1 5

<210> 130
 <211> 305
 <212> DNA
 <213> Aspergillus niger

<220>
 <221> misc_feature
 <222> (186)..(186)
 <223> n is a, c, g, or t

 <400> 130

tcgaacttca	tgttcagtt	cttgttcacg	tagaagccgg	agatgtgaga	ggtgatctgg	60
aactgctcac	cctcggttgg	ggtgacctgg	aggtaaagca	agtgaccctt	ctggcggagg	120
tggtaaggaa	cggggttcca	cggggagaga	gagatggcct	tgacggtctt	gggaagggga	180
gcttcngcgc	gggggaggat	ggtcttgaga	gagggggagc	tagtaatgtc	gtacttggac	240
agggagtgtct	ccttctccga	cgcattcagcc	acctcagcgg	agatggcattc	gtgcagagac	300
agacc						305

<210> 131
 <211> 1488
 <212> DNA
 <213> Cellulomonas strain 69B4

<400> 131

atgacaccac	gaactgtcac	aagagctctg	gctgtggcaa	cagcagctgc	tacactcttg	60
gctggggta	tggcagcaca	agctaacgaa	ccggctccctc	caggatctgc	atcagccccct	120
ccacgattag	ctgaaaaact	tgaccctgac	ttacttgaag	caatggAACG	cgatctgggg	180
ttagatgcag	aggaagcagc	tgcAACgtta	gcttttcagc	atgacgcagc	tgaaacggga	240
gaggctcttg	ctgaggaact	cgacgaagat	ttcgcgggca	cgtgggttga	agatgtatgt	300
ctgtatgttg	caaccactga	tgaagatgtc	gttgaagaag	tgcAAGGCga	aggagcaact	360
gctgtgactg	ttgagcattc	tcttgctgtat	tttagaggcgt	ggaagacgg	tttggatgt	420

gcgctggagg	gtcatgatga	tgtgcctacg	tggtaacgtcg	acgtgcctac	gaattcggt	480
gtcgttgcgt	taaaggcagg	agcgcaggat	gtagctgcag	gacttgttgg	aggcgctgat	540
gtgccatcg	atgcggtcac	ttttgttagaa	acggacaaa	cgcctagaac	gatgttcgac	600
gtaattggag	gcaacgcata	tactattggc	ggccggctca	gatgttctat	cggattcgca	660
gtaaacggtg	gcttcattac	tgccggtcac	tgcggaaagaa	caggagccac	tactgccaat	720
ccgactggca	catttgcagg	tagctcggtt	ccggaaatg	attatgcatt	cgtccgaaca	780
ggggcaggag	taaatttgct	tgcccaagtc	aataactact	cgggcggcag	agtccaaagta	840
gcaggacata	cggccgcacc	agttggatct	gctgtatgcc	gctcaggtag	cactacaggt	900
tggcattgct	gaactatcac	ggcgtgaat	tgcgttgtca	cgtatccaga	ggaaacagtc	960
cgaggactt	tccgcacgac	ggtttgcgc	gaaccagggt	atagcggagg	tagcctttt	1020
gcggaaatc	aagcccaagg	tgtcacgtca	ggtggttctg	gaaattgtcg	gacgggggg	1080
acaacattct	ttcaaccagt	caacccgatt	ttgcaggctt	acggcctgag	aatgattacg	1140
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ggaagcaatg	aaaccattac	gtaccgcgga	aatgctggat	attatcgcta	cgtggtaac	1440
gctgcgtcag	gatcaggagc	ttacacaatg	ggactcaccc	tcccctga		1488

<210> 132
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 132

Asp Asp Asn Asp Pro Ile
1 5

<210> 133
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 133

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gcgttcagca	acatgagcgc	gcaggctgat	gattattcag	ttgttagagga	acatgggcaa	120
ctaatgttata	gtaaacggta	attagtcaat	gaacgaggcg	aacaagttca	gtttaaaaggg	180
atgagttccc	atggtttgc	atggtacggt	caatttgtaa	actatgaaag	catgaaaatgg	240
ctaaagagatg	attggggaaat	aactgtattc	cgagcagcaa	tgtatacctc	ttcaggagga	300
tatattgacg	atccatcagt	aaaggaaaaaa	gtttaaaagaga	ctgtttagggc	tgcgatagac	360
cttggcatat	atgtgatcat	tgattggcat	atcctttcag	acaatgaccc	gaatatataat	420
aaagaagaag	cgaaggattt	ctttgtgaa	atgtcagagt	tgtatggaga	ctatccgaat	480
gtgatatacg	aaattgcaaa	tgaaccgaat	ggtagtgatg	ttacgtggga	caatcaaata	540
aaaccgtatg	cagaagaagt	gattccgggtt	attcgtgaca	atgaccctaa	taacattgtt	600
attgttaggt	caggtacatg	gagtcaggat	gtccatcatg	cagccgataa	tcagcttgca	660
gatcctaacg	tcatgtatgc	atttcatttt	tatgcaggaa	cacatggaca	aaatttacga	720
gaccaagtag	attatgcatt	agatcaagga	gcagcgatat	ttgttagtga	atgggggaca	780
agtgcagcta	caggtgatgg	ttgtgtgttt	ttagatgaag	cacaagtgtg	gattgactt	840
atggatgaaa	gaaatttaag	ctgggccaac	ttgtctctaa	cgcataagga	tgagtcatct	900
gcagcgtaa	tgccaggtgc	aaatccaact	ggtggttgg	cagaggctga	actatctcca	960

tctggtacat ttgtgaggga aaaaataaga gaatcagcat ctgacaacaa tgatccata 1020

<210> 134
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 134

Val Arg Ser Lys Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu
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Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Asp Asp Tyr
20 25 30
Ser Val Val Glu Glu His Gly Gln Leu Ser Ile Ser Asn Gly Glu Leu
35 40 45
Val Asn Glu Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His

50 55 60
Gly Leu Gln Trp Tyr Gly Gln Phe Val Asn Tyr Glu Ser Met Lys Trp
65 70 75 80
Leu Arg Asp Asp Trp Gly Ile Thr Val Phe Arg Ala Ala Met Tyr Thr
85 90 95
Ser Ser Gly Gly Tyr Ile Asp Asp Pro Ser Val Lys Glu Lys Val Lys
100 105 110
Glu Thr Val Glu Ala Ala Ile Asp Leu Gly Ile Tyr Val Ile Ile Asp
115 120 125
Trp His Ile Leu Ser Asp Asn Asp Pro Asn Ile Tyr Lys Glu Glu Ala
130 135 140
Lys Asp Phe Phe Asp Glu Met Ser Glu Leu Tyr Gly Asp Tyr Pro Asn
145 150 155 160
Val Ile Tyr Glu Ile Ala Asn Glu Pro Asn Gly Ser Asp Val Thr Trp
165 170 175
Asp Asn Gln Ile Lys Pro Tyr Ala Glu Glu Val Ile Pro Val Ile Arg
180 185 190
Asp Asn Asp Pro Asn Asn Ile Val Ile Val Gly Thr Gly Thr Trp Ser
195 200 205
Gln Asp Val His His Ala Ala Asp Asn Gln Leu Ala Asp Pro Asn Val
210 215 220
Met Tyr Ala Phe His Phe Tyr Ala Gly Thr His Gly Gln Asn Leu Arg
225 230 235 240
Asp Gln Val Asp Tyr Ala Leu Asp Gln Gly Ala Ala Ile Phe Val Ser
245 250 255
Glu Trp Gly Thr Ser Ala Ala Thr Gly Asp Gly Gly Val Phe Leu Asp
260 265 270
Glu Ala Gln Val Trp Ile Asp Phe Met Asp Glu Arg Asn Leu Ser Trp
275 280 285
Ala Asn Trp Ser Leu Thr His Lys Asp Glu Ser Ser Ala Ala Leu Met
290 295 300
Pro Gly Ala Asn Pro Thr Gly Gly Trp Thr Glu Ala Glu Leu Ser Pro
305 310 315 320
Ser Gly Thr Phe Val Arg Glu Lys Ile Arg Glu Ser Ala Ser Asp Asn
325 330 335
Asn Asp Pro Ile

<210> 135
<211> 30
<212> PRT
<213> Cellulomonas strain 69B4

<400> 135

Met Arg Ser Lys Lys Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr
1 5 10 15
Ala Ala Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
20 25 30

<210> 136
<211> 30
<212> PRT
<213> Cellulomonas strain 69B4

<400> 136

Met Arg Ser Lys Lys Leu Trp Ile Ser Leu Leu Leu Ala Val Ala Thr
1 5 10 15
Ala Ala Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
20 25 30

<210> 137
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 137
ctagcttaggt accatgacac cacgaactgt cacaaggagct

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<210> 138
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 138
gtgtgcaagc tttcagggga gggtgagtcc cattgtgtaa

40

<210> 139
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 139

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<212> DNA	
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<211> 53	
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<210> 144	
<211> 37	
<212> DNA	
<213> Artificial Sequence	
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gtgtgcaagc tttcaagggg aacttccaga gtcagtc	37

<210> 145
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 145
tcatgcaggg taccatgaga agcaagaagt tgtggatcag tttgctgctg gctgtggcaa 60
cagcagctgc taca 74

<210> 146
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 146
gtgtgcaagc tttcagggga gggtgagtcc cattgtgtaa 40

<210> 147
<211> 74 .
<212> DNA
<213> Artificial Sequence

<220>
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<400> 147
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cagcagctgc taca 74

<210> 148
<211> 37
<212> DNA

<213> Artificial Sequence

<220>
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<400> 148
gtgtgcaagc tttcaagggg aacttccaga gtcagtc 37

<210> 149
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 149
ccataccgga tccaaacgaa ccggctcctc caggatct 38

<210> 150
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 150
ctcgagttaa gcttttaagg ggaacttcca gagtcagtc 39

<210> 151
<211> 48
<212> DNA
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<220>
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<400> 151
tgagctgcta gcaaaaaggag agggtaaaga atgacaccac gaactgtc 48

<210> 152
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<212> DNA
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<220>
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<400> 152
cgtacatccc gggtcagggg agggtgagtc ccattg 36

<210> 153
<211> 48
<212> DNA
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<220>
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<400> 153
tgagctgcta gcaaaaaggag agggtaaaga atgacaccac gaactgtc 48

<210> 154
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<220>
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<400> 154

catgcatccc gggtaaggg gaacttccag agtcagtc	38
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<210> 161
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<212> DNA
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<220>
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<400> 162
catgcacccc gggtaaggg gaacttccag agtcagtc 38

<210> 163
<211> 40
<212> DNA
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<220>
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<400> 163
tgcagtctgc tagcaaaagg agaggtaaa gagtgagaag 40

<210> 164
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<220>
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<400> 164

catgcatccc gggtaaggg gaacttccag agtcagtc 38

<210> 165
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<212> DNA
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<220>
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<400> 165
ttatgcgagg ctagcaaaag gagagggtaa agagtgagaa gcaaaaaacg 50

<210> 166
<211> 42
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<213> Artificial Sequence

<220>
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<400> 166
taaagagtga gaagcaaaaa acgcacagtc acgcgggccc tg 42

<210> 167
<211> 35
<212> DNA
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<220>
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<400> 167
gtcctctgtt aacttacggg ctgctgcccg agtcc 35

<210> 168
<211> 41
<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 168
gcaacatgtc tgcgcaggct aacgaaccgg ctcctccagg a 41

<210> 169
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 169
gacatgacat aagcttaagg ggaacttcca gagtc 35

<210>	170	
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<212>	DNA	
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gagccgaatt catataacctg ccgtt		25
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<211>	41	
<212>	DNA	
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gattttctat caaacaagg agaaaaatag accagttgca atccaaacga gagtctaata	240	
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aggacagggtg	ccggcagcgc	tctgggtcat	tttcggcgag	gaccgccttc	gctggagcgc	2160
gacgatgatc	ggcctgtcgc	ttgcgggtatt	cggaatcttgc	cacgcctcg	ctcaagcctt	2220
cgtcaactggt	cccgccacca	aacgtttgg	cgagaagcag	gcattatcg	ccggcatggc	2280
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atggaacggg	ttggcatgga	ttgaggcgcc	gccctatacc	ttatttatgt	tacagtaata	2580
ttgacttttta	aaaaaggatt	gattctaattg	aagaaagcag	acaagtaagc	ctcctaaatt	2640
cacttagat	aaaaatttag	gaggcatatc	aatgaactt	taataaaaatt	gatttagaca	2700
attggaagag	aaaagagata	tttaatcatt	atttgaacca	acaaacgact	tttagtataa	2760
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20 25 30
Pro

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<212> PRT
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<220>
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<400> 174

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20 25 30
Glu Pro Ala Pro
35

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<220>
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<400> 175

Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile
1 5 10 15

Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Asn Glu Pro Ala Pro
20 25 30

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<211> 40

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<211> 40

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CAGAGCTCTT GTGACAGTTTC GTTTCTTCAT TCGGTTCCCT 40

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AATGAAGAAA CGGTGGGGC GAACTGTCAC AAGAGCTCTG 40

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tcctggagga gccgggttcgt tagccgatgc gatcgatgaa ct          42

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<220>
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<400> 183
tgctgtttt atcctttacc ttgtctcc                           28

<210> 184
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<400> 184
agttaagcaa tcagatcttc ttcaggta                          29

<210> 185
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<400> 186
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<210> 187
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<400> 187
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<210> 189
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<400> 189
ccacaagtcc agctgctaca tcctgcgc 28

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<400> 190

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<400> 193
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acaaaaacgg ctttac 120
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<210> 195
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<212> DNA
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<220>
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acgaactgtc acaag 135

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<400> 197
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<400> 203
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<400> 205
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<220>
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<210> 207
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<220>
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<400> 207

aacgaaccgg ctcctccagg atctgcata 30

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ggatct	66	
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ggatct	66	
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20 25 30		
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35 40 45		
Leu Asp Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp		
50 55 60		
Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu		
65 70 75 80		
Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr		

85	90	95
Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala		
100	105	110
Val Glu Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His		
115	120	125
Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu		
130	135	140
Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn		
145	150	155
Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly		
165	170	175
Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu		
180	185	190
Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala		
195	200	205
Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn		
210	215	220
Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr		
225	230	235
Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp		
245	250	255
Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val		
260	265	270
Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala		
275	280	285
Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His		
290	295	300
Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly		
305	310	315
Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp		
325	330	335
Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser		
340	345	350
Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro		
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370	375	380
Ser Gly Ser Ser Pro		
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<400> 215
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29

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<400> 216
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<223> n is a, c, g, or t

<400> 217
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<210> 218
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<210> 230
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<400> 230
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<210> 231
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<210> 345
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35 40 45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
50 55 60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
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Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
85 90 95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
100 105 110
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115 120 125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
130 135 140
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35 40 45
Val Val Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn Asp Tyr Gly
50 55 60
Ile Val Arg Tyr Thr Asp Gly Ser Ser Pro Ala Gly Thr Val Asp Leu
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Tyr Asn Gly Ser Thr Gln Asp Ile Ser Ser Ala Ala Asn Ala Val Val
85 90 95
Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly
100 105 110
Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val

115 120 125
Tyr Asn Met Val Arg Thr Thr Ala Cys Ser Ala Gly Gly Asp Ser Gly
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Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His Ser Gly Ser
145 150 155 160
Ser Gly Cys Ser Gly Thr Ala Gly Ser Ala Ile His Gln Pro Val Thr
165 170 175
Glu Ala Leu Ser Ala Tyr Gly Val Thr Val Tyr
180 185

<210> 626
<211> 185
<212> PRT
<213> Streptomyces griseus

<400> 626

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu
1 5 10 15
Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly
20 25 30
His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser Ala Arg Thr
35 40 45
Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn Asn Asp Tyr
50 55 60
Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp Gly Thr Val
65 70 75 80
Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly Met Ala
85 90 95
Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly Ser Val Thr
100 105 110
Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val Val Tyr Gly
115 120 125

Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Pro
130 135 140
Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly Gly Ser Gly
145 150 155 160
Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val Thr Glu Ala
165 170 175
Leu Val Ala Tyr Gly Val Ser Val Tyr
180 185

<210> 627
<211> 198
<212> PRT

<213> Lysobacter enzymogenes

<400> 627

Ala Asn Ile Val Gly Gly Ile Glu Tyr Ser Ile Asn Asn Ala Ser Leu
1 5 10 15
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Ala Thr Lys Gly Phe Val
20 25 30
Thr Ala Gly His Cys Gly Thr Val Asn Ala Thr Ala Arg Ile Gly Gly

35	40	45
Ala Val Val Gly Thr Phe Ala Ala Arg Val Phe Pro Gly Asn Asp Arg		
50	55	60
Ala Trp Val Ser Leu Thr Ser Ala Gln Thr Leu Leu Pro Arg Val Ala		
65	70	75
Asn Gly Ser Ser Phe Val Thr Val Arg Gly Ser Thr Glu Ala Ala Val		
85	90	95
Gly Ala Ala Val Cys Arg Ser Gly Arg Thr Thr Gly Tyr Gln Cys Gly		
100	105	110
Thr Ile Thr Ala Lys Asn Val Thr Ala Asn Tyr Ala Glu Gly Ala Val		
115	120	125
Arg Gly Leu Thr Gln Gly Asn Ala Cys Met Gly Arg Gly Asp Ser Gly		
130	135	140
Gly Ser Trp Ile Thr Ser Ala Gly Gln Ala Gln Gly Val Met Ser Gly		
145	150	155
Gly Asn Val Gln Ser Asn Gly Asn Asn Cys Gly Ile Pro Ala Ser Gln		
165	170	175
Arg Ser Ser Leu Phe Glu Arg Leu Gln Pro Ile Leu Ser Gln Tyr Gly		
180	185	190
Leu Ser Leu Val Thr Gly		
195		

<210> 628

<211> 191

<212> PRT

<213> Streptomyces fradiae

<400> 628

Ile Ala Gly Gly Glu Ala Ile Tyr Ala Ala Gly Gly Arg Cys Ser		
1	5	10
Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Ala Thr Tyr Ala Leu Thr		
20	25	30
Ala Gly His Cys Thr Glu Ile Ala Ser Thr Trp Tyr Thr Asn Ser Gly		
35	40	45
Gln Thr Ser Leu Leu Gly Thr Arg Ala Gly Thr Ser Phe Pro Gly Asn		
50	55	60
Asp Tyr Gly Leu Ile Arg His Ser Asn Ala Ser Ala Ala Asp Gly Arg		
65	70	75
Val Tyr Leu Tyr Asn Gly Ser Tyr Arg Asp Ile Thr Gly Ala Gly Asn		
85	90	95
Ala Tyr Val Gly Gln Thr Val Gln Arg Ser Gly Ser Thr Thr Gly Leu		
100	105	110
His Ser Gly Arg Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly		
115	120	125
Gly Asp Ile Val Ser Gly Leu Ile Gln Thr Asn Val Cys Ala Glu Pro		
130	135	140
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Ser Thr Ala Leu Gly Leu		
145	150	155
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe		
165	170	175
Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Ile Leu		
180	185	190

<210> 629

<211> 181

<212> PRT

<213> Streptomyces griseus

<400> 629

Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu
1 5 10 15
Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly
20 25 30
His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly
35 40 45
Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His Ser Asn Pro
50 55 60
Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp
65 70 75 80
Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser
85 90 95
Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala
100 105 110
Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr
115 120 125
Asn Val Cys Ala Gln Pro Gly Asp Ser Gly Gly Ser Leu Phe Ala Gly
130 135 140
Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145 150 155 160
Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr
165 170 175
Gly Ala Thr Val Leu
180

<210> 630

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 630

Pro Arg Thr Met Phe Asp
1 5

<210> 631

<211> 10

<212> PRT

<213> Cellulomonas strain 69B4

<400> 631

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
1 5 10

<210> 632

<211> 9

<212> PRT

<213> Cellulomonas strain 69B4

<400> 632

Thr Ala Asn Pro Thr Gly Thr Phe Ala
1 5

<210> 633

<211> 12

<212> PRT

<213> Cellulomonas strain 69B4

<400> 633

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
1 5 10

<210> 634

<211> 14

<212> PRT

<213> Cellulomonas strain 69B4

<400> 634

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val
1 5 10

<210> 635

<211> 10

<212> PRT

<213> Cellulomonas strain 69B4

<400> 635

Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
1 5 10

<210> 636

<211> 9

<212> PRT

<213> Cellulomonas strain 69B4

<400> 636

Phe Phe Gln Pro Val Asn Pro Ile Leu
1 5

<210> 637

<211> 11

<212> PRT

<213> Cellulomonas strain 69B4

<400> 637

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala
1 5 10

<210> 638
<211> 13
<212> PRT
<213> Cellulomonas strain 69B4

<400> 638

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly
1 5 10

<210> 639
<211> 255
<212> PRT
<213> Streptogrisin C

<400> 639

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg
1 5 10 15
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala
20 25 30
Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Asn Gly Val Asn
35 40 45
Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp
50 55 60
Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val
65 70 75 80
Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser
85 90 95
Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
100 105 110
Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly
115 120 125
Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp
130 135 140
Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser
145 150 155 160
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro
165 170 175
Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly
180 185 190
Gly Gly Thr Pro Thr Asp Pro Pro Thr Thr Pro Pro Thr Asp Ser Pro
195 200 205
Gly Gly Thr Trp Ala Val Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val
210 215 220
Thr Tyr Gly Gly Ala Thr Tyr Arg Cys Leu Gln Ala His Thr Ala Gln
225 230 235 240
Pro Gly Trp Thr Pro Ala Asp Val Pro Ala Leu Trp Gln Arg Val
245 250 255

<210> 640
<211> 185
<212> PRT
<213> Streptogrisin B

<400> 640

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu
1 5 10 15
Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly

20 25 30
His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser Ala Arg Thr
35 40 45
Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn Asn Asp Tyr
50 55 60
Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp Gly Thr Val
65 70 75 80
Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly Met Ala
85 90 95
Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly Ser Val Thr
100 105 110
Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val Val Tyr Gly
115 120 125
Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Pro
130 135 140
Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly Gly Ser Gly
145 150 155 160
Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val Thr Glu Ala
165 170 175
Leu Ser Ala Tyr Gly Val Ser Val Tyr
180 185

<210> 641

<211> 181

<212> PRT

<213> Streptogrisin A

<400> 641

Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu
1 5 10 15
Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly
20 25 30
His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly
35 40 45
Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Arg His Ser Asn Pro
50 55 60
Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp
65 70 75 80
Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser
85 90 95
Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala
100 105 110
Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr
115 120 125
Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Ser Leu Phe Ala Gly
130 135 140
Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145 150 155 160
Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr
165 170 175
Gly Ala Thr Val Leu

180

<210> 642
<211> 188
<212> PRT
<213> Streptogrisin D

<400> 642

Ile Ala Gly Gly Asp Ala Ile Trp Gly Ser Gly Ser Arg Cys Ser Leu
1 5 10 15
Gly Phe Asn Val Val Lys Gly Gly Glu Pro Tyr Phe Leu Thr Ala Gly
20 25 30
His Cys Thr Glu Ser Val Thr Ser Trp Ser Asp Thr Gln Gly Gly Ser
35 40 45
Glu Ile Gly Ala Asn Glu Gly Ser Ser Phe Pro Glu Asn Asp Tyr Gly
50 55 60
Leu Val Lys Tyr Thr Ser Asp Thr Ala His Pro Ser Glu Val Asn Leu
65 70 75 80
Tyr Asp Gly Ser Thr Gln Ala Ile Thr Gln Ala Gly Asp Ala Thr Val
85 90 95
Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val His Asp Gly

100 105 110
Glu Val Thr Ala Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly Asp Ile
115 120 125
Val Asn Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser
130 135 140
Gly Gly Ala Leu Phe Ala Gly Asp Thr Ala Leu Gly Leu Thr Ser Gly
145 150 155 160
Gly Ser Gly Asp Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
165 170 175
Pro Glu Ala Leu Ala Ala Tyr Gly Ala Glu Ile Gly
180 185

<210> 643
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> VARIANT
<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (12)..(12)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (22)..(23)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (25)..(27)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (37)..(38)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (43)..(51)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (55)..(56)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (62)..(62)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (73)..(79)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (82)..(82)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (84)..(84)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (86)..(87)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (89)..(89)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (92)..(92)

<223> Xaa can be any naturally occurring amino acid

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<220>
<221> VARIANT
<222> (95)..(95)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (97)..(97)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (100)..(100)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (103)..(103)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (111)..(111)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (113)..(113)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (127)..(127)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (129)..(129)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (132)..(132)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (155)..(155)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (179)..(179)
<223> Xaa can be any naturally occurring amino acid

<220>
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<221> VARIANT
<222> (191)..(198)
<223> Xaa can be any naturally occurring amino acid

<400> 643

Ile Ala Gly Gly Asp Ala Ile Tyr Xaa Xaa Gly Xaa Ser Arg Cys Ser
1 5 10 15
Leu Gly Phe Asn Val Xaa Xaa Gly Xaa Xaa Xaa Tyr Phe Leu Thr Ala
20 25 30
Gly His Cys Thr Xaa Xaa Gly Thr Thr Trp Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Xaa Ile Gly Thr Xaa Xaa Gly Ser Ser Phe Pro Xaa Asn Asp
50 55 60
Tyr Gly Ile Val Arg Tyr Thr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
65 70 75 80
Asn Xaa Tyr Xaa Gly Xaa Xaa Gln Xaa Ile Thr Xaa Ala Gly Xaa Ala
85 90 95
Xaa Val Gly Xaa Ala Val Xaa Arg Ser Gly Ser Thr Thr Gly Xaa His
100 105 110
Xaa Gly Ser Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Xaa Gly
115 120 125
Xaa Ile Val Xaa Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly
130 135 140
Asp Ser Gly Gly Ser Leu Phe Ala Gly Ser Xaa Ala Leu Gly Leu Thr
145 150 155 160
Ser Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln
165 170 175
Pro Val Xaa Glu Ala Leu Ser Ala Tyr Gly Leu Thr Val Ile Xaa Xaa
180 185 190
Xaa Xaa Xaa Xaa Xaa
195

<210> 644

<211> 513

<212> PRT

<213> Thermus aquaticus

<400> 644

Met Arg Lys Thr Tyr Trp Leu Met Ala Leu Phe Ala Val Leu Val Leu
1 5 10 15
Gly Gly Cys Gln Met Ala Ser Arg Ser Asp Pro Thr Pro Thr Leu Ala
20 25 30
Glu Ala Phe Trp Pro Lys Glu Ala Pro Val Tyr Gly Leu Asp Asp Pro
35 40 45
Glu Ala Ile Pro Gly Arg Tyr Ile Val Val Phe Lys Lys Gly Lys Gly
50 55 60
Gln Ser Leu Leu Gln Gly Gly Ile Thr Thr Leu Gln Ala Arg Leu Ala
65 70 75 80
Pro Gln Gly Val Val Val Thr Gln Ala Tyr Thr Gly Ala Leu Gln Gly
85 90 95
Phe Ala Ala Glu Met Ala Pro Gln Ala Leu Glu Ala Phe Arg Gln Ser
100 105 110
Pro Asp Val Glu Phe Ile Glu Ala Asp Lys Val Val Arg Ala Trp Ala
115 120 125
Thr Gln Ser Pro Ala Pro Trp Gly Leu Asp Arg Ile Asp Gln Arg Asp

130	135	140
Leu Pro Leu Ser Asn Ser Tyr Thr Tyr Thr Ala Thr Gly Arg Gly Val		
145	150	155 160
Asn Val Tyr Val Ile Asp Thr Gly Ile Arg Thr Thr His Arg Glu Phe		
165	170	175
Gly Gly Arg Ala Arg Val Gly Tyr Asp Ala Leu Gly Gly Asn Gly Gln		
180	185	190
Asp Cys Asn Gly His Gly Thr His Val Ala Gly Thr Ile Gly Gly Val		
195	200	205
Thr Tyr Gly Val Ala Lys Ala Val Asn Leu Tyr Ala Val Arg Val Leu		
210	215	220
Asp Cys Asn Gly Ser Gly Ser Thr Ser Gly Val Ile Ala Gly Val Asp		
225	230	235 240
Trp Val Thr Arg Asn His Arg Arg Pro Ala Val Ala Asn Met Ser Leu		
245	250	255
Gly Gly Gly Val Ser Thr Ala Leu Asp Asn Ala Val Lys Asn Ser Ile		
260	265	270
Ala Ala Gly Val Val Tyr Ala Val Ala Ala Gly Asn Asp Asn Ala Asn		
275	280	285
Ala Cys Asn Tyr Ser Pro Ala Arg Val Ala Glu Ala Leu Thr Val Gly		
290	295	300
Ala Thr Thr Ser Ser Asp Ala Arg Ala Ser Phe Ser Asn Tyr Gly Ser		
305	310	315 320
Cys Val Asp Leu Phe Ala Pro Gly Ala Ser Ile Pro Ser Ala Trp Tyr		
325	330	335
Thr Ser Asp Thr Ala Thr Gln Thr Leu Asn Gly Thr Ser Met Ala Thr		
340	345	350
Pro His Val Ala Gly Val Ala Ala Leu Tyr Leu Glu Gln Asn Pro Ser		
355	360	365
Ala Thr Pro Ala Ser Val Ala Ser Ala Ile Leu Asn Gly Ala Thr Thr		
370	375	380
Gly Arg Leu Ser Gly Ile Gly Ser Gly Ser Pro Asn Arg Leu Leu Tyr		
385	390	395 400
Ser Leu Leu Ser Ser Gly Ser Gly Ser Thr Ala Pro Cys Thr Ser Cys		
405	410	415
Ser Tyr Tyr Thr Gly Ser Leu Ser Gly Pro Gly Asp Tyr Asn Phe Gln		
420	425	430
Pro Asn Gly Thr Tyr Tyr Ser Pro Ala Gly Thr His Arg Ala Trp		
435	440	445
Leu Arg Gly Pro Ala Gly Thr Asp Phe Asp Leu Tyr Leu Trp Arg Trp		
450	455	460
Asp Gly Ser Arg Trp Leu Thr Val Gly Ser Ser Thr Gly Pro Thr Ser		
465	470	475 480
Glu Glu Ser Leu Ser Tyr Ser Gly Thr Ala Gly Tyr Tyr Leu Trp Arg		
485	490	495
Ile Tyr Ala Tyr Ser Gly Ser Gly Met Tyr Glu Phe Trp Leu Gln Arg		
500	505	510
Pro		

<210> 645
<211> 495
<212> PRT
<213> Cellulomonas strain 69B4

<400> 645

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
1 5 10 15
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu Pro Ala
20 25 30
Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala Glu Lys Leu Asp
35 40 45
Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp Ala Glu
50 55 60
Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu Thr Gly
65 70 75 80
Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr Trp Val
85 90 95
Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala Val Glu
100 105 110
Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His Ser Leu
115 120 125
Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu Glu Gly
130 135 140
His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn Ser Val
145 150 155 160
Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly Leu Val
165 170 175
Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu Thr Asp
180 185 190
Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
195 200 205
Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn Gly Gly
210 215 220
Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn
225 230 235 240
Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
245 250 255
Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val Asn Asn
260 265 270
Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala Pro Val
275 280 285
Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
290 295 300
Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly Thr Val
305 310 315 320
Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
325 330 335
Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly
340 345 350
Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Asn
355 360 365
Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr Thr Asp Ser Gly
370 375 380
Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly Tyr Ala Arg Thr
385 390 395 400
Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala Gln Pro Asn Gly
405 410 415
Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser Val Cys Leu Asn
420 425 430
Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln Arg Trp Asn Gly
435 440 445
Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro Gly Ser Asn Glu

450	455	460
Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg Tyr Val Val Asn		
465	470	475
Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu Thr Leu Pro		480
485	490	495

<210> 646
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> VARIANT
<222> (3) .. (509)
<223> Xaa can be any naturally occurring amino acid

<400> 646

Met Ala Xaa Xaa Ala Xaa Xaa Leu Leu Ala Gly Xaa Xaa Xaa Ala Xaa		
1	5	10
Xaa Xaa Asp Pro Xaa Pro Xaa Xaa Ala Xaa Ala Xaa Xaa Pro Lys Xaa		
20	25	30
Ala Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Glu Ala Ile Xaa Xaa Xaa Xaa		
35	40	45
Xaa Leu Xaa Xaa Xaa Xaa Ala Xaa Ala Xaa Xaa Xaa Gln Xaa Xaa		
50	55	60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Ala Xaa Xaa Xaa Xaa Xaa Leu Xaa		
65	70	75
Xaa Xaa Phe Xaa Gly Xaa		
85	90	95
Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Glu Xaa Xaa Xaa		
100	105	110
Ala Xaa Xaa Val Xaa Xaa Ala Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
115	120	125
Xaa Leu Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Tyr		
130	135	140
Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Val Xaa Xaa Ile Xaa Xaa		
145	150	155
Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Val Xaa		
165	170	175
Xaa Asp Ala Leu Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa		
180	185	190
Xaa Met Xaa Xaa Xaa Ile Gly Gly Xaa Xaa Tyr Xaa Ile Ala Xaa Xaa		
195	200	205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Ala		
210	215	220
Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa		
225	230	235
Xaa Xaa Ala Xaa Xaa Xaa Xaa Ser Xaa Ala Gly Xaa Xaa Xaa Xaa Ala		
245	250	255
Xaa Asp Xaa Ala Xaa Xaa Xaa Ser Xaa Ala Ala Xaa Xaa Xaa Xaa Xaa		
260	265	270
Xaa Xaa Xaa Asn Xaa Xaa Ala Asn Xaa Xaa Asn Tyr Ser Xaa Ala		
275	280	285

Arg Val Xaa Xaa Ala Xaa Xaa Xaa Ala Ala Xaa Xaa Xaa Ser Xaa Xaa
 290 295 300
 Xaa Xaa Ser Xaa Ser Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 305 310 315 320
 Xaa Ala Xaa Xaa Xaa Ser Xaa Xaa Tyr Xaa Xaa Xaa Thr Xaa Xaa Xaa
 325 330 335
 Xaa Ile Xaa Xaa Thr Xaa Xaa Ala Xaa Pro Xaa Xaa Ala Gly Xaa Ala
 340 345 350
 Xaa Leu Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Thr Xaa Ala Xaa Xaa Ala
 355 360 365
 Xaa Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 370 375 380
 Xaa Xaa Ala Xaa Xaa Xaa Xaa Leu Xaa Ser Xaa Xaa Ser Xaa Gly Ser
 385 390 395 400
 Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Cys Ser Xaa Tyr Xaa Xaa Ser Xaa
 405 410 415
 Ser Gly Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Gln Pro Asn Gly Ser
 420 425 430
 Tyr Xaa Xaa Xaa Xaa Ala Gly Thr His Xaa Xaa Xaa Leu Xaa Gly
 435 440 445
 Pro Ala Gly Xaa Asp Phe Asp Leu Tyr Leu Xaa Arg Trp Xaa Gly Ser
 450 455 460
 Xaa Trp Leu Thr Val Ala Xaa Ser Thr Xaa Pro Xaa Ser Xaa Glu Ser
 465 470 475 480
 Ile Ser Tyr Xaa Gly Xaa Ala Gly Tyr Tyr Xaa Trp Xaa Ile Xaa Ala
 485 490 495
 Xaa Ser Gly Ser Gly Xaa Tyr Xaa Xaa Leu Xaa Xaa Pro
 500 505 510

<210> 647
 <211> 190
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<220>
 <221> VARIANT
 <222> (6)..(188)
 <223> Xaa can be any naturally occurring amino acid

<400> 647

Asp Val Ile Gly Gly Xaa Xaa Tyr Xaa Ile Xaa Xaa Xaa Xaa Arg Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Cys Ser Ile Gly Phe Ala Val Xaa Gly Gly Phe Val
 20 25 30
 Thr Ala Gly His Cys Gly Arg Xaa Gly Ala Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Thr Ser Xaa Pro Xaa Gly Thr Phe Xaa Gly Ser Ser Phe Pro Gly Asn
 50 55 60
 Asp Tyr Ala Trp Val Gln Val Ala Ser Gly Asn Thr Pro Val Gly Ala
 65 70 75 80
 Val Asn Asn Tyr Ser Gly Gly Thr Val Xaa Val Ala Gly Ser Thr Xaa
 85 90 95
 Ala Ala Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp

100	105	110
Arg Cys Gly Thr Ile Xaa Ala Tyr Asn Ala Ser Val Xaa Tyr Ala Glu		
115	120	125
Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly		
130	135	140
Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr		
145	150	155
Ser Gly Gly Ser Gly Asn Cys Xaa Xaa Gly Gly Thr Thr Tyr Phe Gln		
165	170	175
Pro Val Asn Xaa Xaa Leu Xaa Xaa Tyr Gly Leu Xaa Leu Val		
180	185	190

<210> 648

<211> 368

<212> PRT

<213> Thermobifida fusca

<400> 648

Met Asn His Ser Ser Arg Arg Thr Thr Ser Leu Leu Phe Thr Ala Ala		
1	5	10
		15
Leu Ala Ala Thr Ala Leu Val Ala Ala Thr Thr Pro Ala Ser Ala Gln		
20	25	30
Glu Leu Ala Leu Lys Arg Asp Leu Gly Leu Ser Asp Ala Glu Val Ala		
35	40	45
Glu Leu Arg Ala Ala Glu Ala Val Glu Leu Glu Glu Glu Leu		
50	55	60
Arg Asp Ser Leu Gly Ser Asp Phe Gly Gly Val Tyr Leu Asp Ala Asp		
65	70	75
		80
Thr Thr Glu Ile Thr Val Ala Val Thr Asp Pro Ala Ala Val Ser Arg		
85	90	95
Val Asp Ala Asp Asp Val Thr Val Asp Val Val Asp Phe Gly Glu Thr		
100	105	110
Ala Leu Asn Asp Phe Val Ala Ser Leu Asn Ala Ile Ala Asp Thr Ala		
115	120	125
Asp Pro Lys Val Thr Gly Trp Tyr Thr Asp Leu Glu Ser Asp Ala Val		
130	135	140
Val Ile Thr Thr Leu Arg Gly Gly Thr Pro Ala Ala Glu Glu Leu Ala		
145	150	155
		160
Glu Arg Ala Gly Leu Asp Glu Arg Ala Val Arg Ile Val Glu Glu Asp		
165	170	175
Glu Glu Pro Gln Ser Leu Ala Ala Ile Ile Gly Gly Asn Pro Tyr Tyr		
180	185	190
Phe Gly Asn Tyr Arg Cys Ser Ile Gly Phe Ser Val Arg Gln Gly Ser		
195	200	205
Gln Thr Gly Phe Ala Thr Ala Gly His Cys Gly Ser Thr Gly Thr Arg		
210	215	220
Val Ser Ser Pro Ser Gly Thr Val Ala Gly Ser Tyr Phe Pro Gly Arg		
225	230	235
		240
Asp Met Gly Trp Val Arg Ile Thr Ser Ala Asp Thr Val Thr Pro Leu		
245	250	255
Val Asn Arg Tyr Asn Gly Gly Thr Val Thr Val Thr Gly Ser Gln Glu		
260	265	270
Ala Ala Thr Gly Ser Ser Val Cys Arg Ser Gly Ala Thr Thr Gly Trp		
275	280	285
Arg Cys Gly Thr Ile Gln Ser Lys Asn Gln Thr Val Arg Tyr Ala Glu		
290	295	300

Gly Thr Val Thr Gly Leu Thr Arg Thr Thr Ala Cys Ala Glu Gly Gly
 305 310 315 320
 Asp Ser Gly Gly Pro Trp Leu Thr Gly Ser Gln Ala Gln Gly Val Thr
 325 330 335
 Ser Gly Gly Thr Gly Asp Cys Arg Ser Gly Gly Ile Thr Phe Phe Gln
 340 345 350
 Pro Ile Asn Pro Leu Leu Ser Tyr Phe Gly Leu Gln Leu Val Thr Gly
 355 360 365

<210> 649
 <211> 382
 <212> PRT
 <213> Streptomyces spp.

<400> 649

Met Arg His Thr Gly Arg Asn Ala Ile Gly Ala Ala Ile Ala Ala Ser
 1 5 10 15
 Ala Leu Ala Phe Ala Leu Val Pro Ser Gln Ala Ala Asn Asp Thr
 20 25 30
 Leu Thr Glu Arg Ala Glu Ala Ala Val Ala Asp Leu Pro Ala Gly Val
 35 40 45
 Leu Asp Ala Met Glu Arg Asp Leu Gly Leu Ser Glu Gln Glu Ala Gly
 50 55 60
 Leu Lys Leu Val Ala Glu His Asp Ala Ala Leu Leu Gly Glu Thr Leu
 65 70 75 80
 Ser Ala Asp Leu Asp Ala Phe Ala Gly Ser Trp Leu Ala Glu Gly Thr
 85 90 95
 Glu Leu Val Val Ala Thr Thr Ser Glu Ala Glu Ala Ala Glu Ile Thr
 100 105 110
 Glu Ala Gly Ala Thr Ala Glu Val Val Asp His Thr Leu Ala Glu Leu
 115 120 125
 Asp Ser Val Lys Asp Ala Leu Asp Thr Ala Ala Glu Ser Tyr Asp Thr
 130 135 140
 Thr Asp Ala Pro Val Trp Tyr Val Asp Val Thr Thr Asn Gly Val Val
 145 150 155 160
 Leu Leu Thr Ser Asp Val Thr Glu Ala Glu Gly Phe Val Glu Ala Ala
 165 170 175
 Gly Val Asn Ala Ala Ala Val Asp Ile Gln Thr Ser Asp Glu Gln Pro
 180 185 190
 Gln Ala Phe Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Met Gly Gly
 195 200 205
 Gly Arg Cys Ser Val Gly Phe Ser Val Thr Gln Gly Ser Thr Pro Gly
 210 215 220
 Phe Ala Thr Ala Gly His Cys Gly Thr Val Gly Thr Ser Thr Thr Gly
 225 230 235 240
 Tyr Asn Gln Ala Ala Gln Gly Thr Phe Glu Glu Ser Ser Phe Pro Gly
 245 250 255
 Asp Asp Met Ala Trp Val Ser Val Asn Ser Asp Trp Asn Thr Thr Pro
 260 265 270
 Thr Val Asn Glu Gly Glu Val Thr Val Ser Gly Ser Thr Glu Ala Ala
 275 280 285
 Val Gly Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys
 290 295 300
 Gly Thr Ile Gln Gln His Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr
 305 310 315 320
 Ile Thr Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser

	325	330	335												
Gly	Gly	Ser	Tyr	Ile	Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly
	340					345								350	
Gly	Ser	Gly	Asn	Cys	Thr	Ser	Gly	Gly	Thr	Thr	Tyr	His	Gln	Pro	Ile
	355					360						365			
Asn	Pro	Leu	Leu	Ser	Ala	Tyr	Gly	Leu	Asp	Leu	Val	Thr	Gly		
	370					375					380				

<210> 650

<211> 388

<212> PRT

<213> Streptomyces spp.

<400> 650

Met	Arg	Leu	Lys	Gly	Arg	Thr	Val	Ala	Ile	Gly	Ser	Ala	Leu	Ala	Ala	
1															15	
Ser	Ala	Leu	Ala	Leu	Ser	Leu	Val	Pro	Ala	Asn	Ala	Ser	Ser	Glu	Leu	
Pro	Ser	Ala	Glu	Thr	Ala	Lys	Ala	Asp	Ala	Leu	Val	Glu	Gln	Leu	Pro	
Ala	Gly	Met	Val	Asp	Ala	Met	Glu	Arg	Asp	Leu	Gly	Val	Pro	Ala	Ala	
50																
55																
Gl	u	Val	Gly	Asn	Gln	Leu	Val	Ala	Glu	His	Glu	Ala	Ala	Val	Leu	Glu
65																
70																
75																
80																
Glu	Ser	Leu	Ser	Glu	Asp	Leu	Ser	Gly	Tyr	Ala	Gly	Ser	Trp	Ile	Val	
85																
90																
95																
Glu	Gly	Thr	Ser	Glu	His	Val	Val	Ala	Thr	Thr	Asp	Arg	Ala	Glu	Ala	
100																
105																
110																
Ala	Glu	Ile	Thr	Ala	Ala	Gly	Ala	Thr	Ala	Thr	Val	Val	Glu	His	Ser	
115																
120																
125																
Leu	Ala	Glu	Leu	Glu	Ala	Val	Lys	Asp	Ile	Leu	Asp	Glu	Ala	Ala	Thr	
130																
135																
140																
Ala	Asn	Pro	Glu	Asp	Ala	Ala	Pro	Val	Trp	Tyr	Val	Asp	Val	Thr	Thr	
145																
150																
155																
160																
Asn	Glu	Val	Val	Val	Leu	Ala	Ser	Asp	Val	Pro	Ala	Ala	Glu	Ala	Phe	
165																
170																
175																
Val	Ala	Ala	Ser	Gly	Ala	Asp	Ala	Ser	Thr	Val	Arg	Val	Glu	Arg	Ser	
180																
185																
190																
Asp	Glu	Ser	Pro	Gln	Pro	Phe	Tyr	Asp	Leu	Val	Gly	Gly	Asp	Ala	Tyr	
195																
200																
205																
Tyr	Ile	Gly	Asn	Gly	Arg	Cys	Ser	Ile	Gly	Phe	Ser	Val	Arg	Gln	Gly	
210																
215																
220																
Ser	Thr	Pro	Gly	Phe	Val	Thr	Ala	Gly	His	Cys	Gly	Ser	Val	Gly	Asn	
225																
230																
235																
240																
Ala	Thr	Thr	Gly	Phe	Asn	Arg	Val	Ser	Gln	Gly	Thr	Phe	Arg	Gly	Ser	
245																
250																
255																
Trp	Phe	Pro	Gly	Arg	Asp	Met	Ala	Trp	Val	Ala	Val	Asn	Ser	Asn	Trp	
260																
265																
270																
Thr	Pro	Thr	Ser	Leu	Val	Arg	Asn	Ser	Gly	Ser	Gly	Val	Arg	Val	Thr	
275																
280																
285																
Gly	Ser	Thr	Gln	Ala	Thr	Val	Gly	Ser	Ser	Ile						

Ala Gln Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly Thr Gln Ala
340 345 350
Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ile Gly Gly Thr
355 360 365
Thr Phe His Gln Pro Val Asn Pro Ile Leu Ser Gln Tyr Gly Leu Thr
370 375 380
Leu Val Arg Ser
385

<210> 651
<211> 458
<212> PRT
<213> Streptomyces lividans

<400> 651

Met Val Gly Arg His Ala Ala Arg Ser Arg Arg Ala Ala Leu Thr Ala
1 5 10 15
Leu Gly Ala Leu Val Leu Thr Ala Leu Pro Ser Ala Ala Ser Ala Ala
20 25 30
Pro Pro Pro Val Pro Gly Pro Arg Pro Ala Val Ala Arg Thr Pro Asp
35 40 45
Ala Ala Thr Ala Pro Ala Arg Met Leu Ser Ala Met Glu Arg Asp Leu
50 55 60
Arg Leu Ala Pro Gly Gln Ala Ala Arg Pro Val Asn Glu Ala Glu
65 70 75 80
Ala Gly Thr Arg Ala Gly Met Leu Arg Asn Thr Leu Gly Asp Arg Phe
85 90 95
Ala Gly Ala Trp Val Ser Gly Ala Thr Ser Ala Glu Leu Thr Val Ala
100 105 110
Thr Thr Asp Ala Ala Asp Thr Ala Ala Ile Glu Ala Gln Gly Ala Lys
115 120 125
Ala Ala Val Val Gly Arg Asn Leu Ala Glu Leu Arg Ala Val Lys Glu
130 135 140
Lys Leu Asp Ala Ala Ala Val Arg Thr Arg Thr Arg Gln Thr Pro Val
145 150 155 160
Trp Tyr Val Asp Val Lys Thr Asn Arg Val Thr Val Gln Ala Thr Gly
165 170 175
Ala Ser Ala Ala Ala Ala Phe Val Glu Ala Ala Gly Val Pro Ala Ala
180 185 190
Asp Val Gly Val Arg Val Ser Pro Asp Gln Pro Arg Val Leu Glu Asp
195 200 205
Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg Cys Ser
210 215 220
Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala Thr Ala
225 230 235 240
Gly His Cys Gly Asp Pro Gly Ala Thr Thr Gly Tyr Asn Glu Ala
245 250 255
Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp Met Ala
260 265 270
Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Lys Ala
275 280 285
Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala Leu Val
290 295 300
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
305 310 315 320
Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly Thr Val

325	330	335
Asp Gly Leu Thr Gly Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly		
340	345	350
Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser Gly Gly		
355	360	365
Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro Val Asn		
370	375	380
Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser Ala Ala		
385	390	395
Thr Gln Thr Pro Ala Pro Gln Asp Asn Ala Ala Ala Asp Ala Trp Thr		
405	410	415
Ala Gly Arg Val Tyr Glu Val Gly Thr Thr Val Ser Tyr Asp Gly Val		
420	425	430
Arg Tyr Arg Cys Leu Gln Ser His Gln Ala Gln Gly Val Gly Ser Pro		
435	440	445
Ala Ser Val Pro Ala Leu Trp Gln Arg Val		
450	455	

<210> 652

<211> 458

<212> PRT

<213> Streptomyces coelicolor A3(2)

<400> 652

Met Val Gly Arg His Ala Ala Arg Ser Arg Arg Ala Ala Leu Thr Ala		
1	5	10
Leu Gly Ala Leu Val Leu Thr Ala Leu Pro Ser Ala Ala Ser Ala Ala		
20	25	30
Pro Pro Pro Val Pro Gly Pro Arg Pro Ala Val Ala Arg Thr Pro Asp		
35	40	45
Ala Ala Thr Ala Pro Ala Arg Met Leu Ser Ala Met Glu Arg Asp Leu		
50	55	60
Arg Leu Ala Pro Gly Gln Ala Ala Ala Arg Leu Val Asn Glu Ala Glu		
65	70	75
Ala Gly Thr Arg Ala Gly Met Leu Arg Asn Thr Leu Gly Asp Arg Phe		
85	90	95
Ala Gly Ala Trp Val Ser Gly Ala Thr Ser Ala Glu Leu Thr Val Ala		
100	105	110
Thr Thr Asp Ala Ala Asp Thr Ala Ala Ile Glu Ala Gln Gly Ala Lys		
115	120	125
Ala Ala Val Val Gly Arg Asn Leu Ala Glu Leu Arg Ala Val Lys Glu		
130	135	140
Lys Leu Asp Ala Ala Ala Val Arg Thr Arg Thr Arg Gln Thr Pro Val		
145	150	155
Trp Tyr Val Asp Val Lys Thr Asn Arg Val Thr Val Gln Ala Thr Gly		
165	170	175
Ala Ser Ala Ala Ala Ala Phe Val Glu Ala Ala Gly Val Pro Ala Ala		
180	185	190
Asp Val Gly Val Arg Val Ser Pro Asp Gln Pro Arg Val Leu Glu Asp		
195	200	205
Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg Cys Ser		
210	215	220
Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala Thr Ala		
225	230	235
Gly His Cys Gly Asp Pro Gly Ala Thr Thr Thr Gly Tyr Asn Glu Ala		
245	250	255

Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp Met Ala
 260 265 270
 Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Lys Ala
 275 280 285
 Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala Leu Val
 290 295 300
 Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
 305 310 315 320
 Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly Thr Val
 325 330 335
 Asp Gly Leu Thr Glu Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
 340 345 350
 Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser Gly Gly
 355 360 365
 Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro Val Asn
 370 375 380
 Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser Ala Ala
 385 390 395 400
 Thr Gln Thr Pro Ala Pro Gln Asp Asn Ala Ala Ala Asp Ala Trp Thr
 405 410 415
 Ala Gly Arg Val Tyr Glu Val Gly Thr Thr Val Ser Tyr Asp Gly Val
 420 425 430
 Arg Tyr Arg Cys Leu Gln Ser His Gln Ala Gln Gly Val Gly Ser Pro
 435 440 445
 Ala Ser Val Pro Ala Leu Trp Gln Arg Val
 450 455

<210> 653
 <211> 456
 <212> PRT

<213> Streptomyces avermitilis MA-4680

<400> 653

Met Val His Arg His Val Gly Ala Gly Cys Ala Gly Leu Ser Val Leu
 1 5 10 15
 Ala Thr Leu Val Leu Thr Gly Leu Pro Ala Ala Ala Ile Glu Pro
 20 25 30
 Pro Gly Pro Ala Pro Ala Pro Ser Ala Val Gln Pro Leu Gly Ala Gly
 35 40 45
 Asn Pro Ser Thr Ala Val Leu Gly Ala Leu Gln Arg Asp Leu His Leu
 50 55 60
 Thr Asp Thr Gln Ala Lys Thr Arg Leu Val Asn Glu Met Glu Ala Gly
 65 70 75 80
 Thr Arg Ala Gly Arg Leu Gln Asn Ala Leu Gly Lys His Phe Ala Gly
 85 90 95
 Ala Trp Val His Gly Ala Ala Ser Ala Asp Leu Thr Val Ala Thr Thr
 100 105 110
 His Ala Thr Asp Ile Pro Ala Ile Thr Ala Gly Gly Ala Thr Ala Val
 115 120 125
 Val Val Lys Thr Gly Leu Asp Asp Leu Lys Gly Ala Lys Lys Lys Leu
 130 135 140
 Asp Ser Ala Val Ala His Gly Gly Thr Ala Val Asn Thr Pro Val Arg
 145 150 155 160
 Tyr Val Asp Val Arg Thr Asn Arg Val Thr Leu Gln Ala Arg Ser Arg
 165 170 175
 Ala Ala Ala Asp Ala Leu Ile Ala Ala Gly Val Asp Ser Gly Leu

	180	185	190
Val Asp Val Lys Val Ser Glu Asp Arg Pro Arg Ala Leu Phe Asp Ile			
195	200	205	
Arg Gly Gly Asp Ala Tyr Tyr Ile Asp Asn Thr Ala Arg Cys Ser Val			
210	215	220	
Gly Phe Ser Val Thr Lys Gly Asn Gln Gln Gly Phe Ala Thr Ala Gly			
225	230	235	240
His Cys Gly Arg Ala Gly Ala Pro Thr Ala Gly Phe Asn Glu Val Ala			
245	250	255	
Gln Gly Thr Val Gln Ala Ser Val Phe Pro Gly His Asp Met Ala Trp			
260	265	270	
Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Ala Gly Ala			
275	280	285	
Ala Gly Gln Asn Val Ser Ile Ala Gly Ser Val Gln Ala Ile Val Gly			
290	295	300	
Ala Ala Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr			
305	310	315	320
Val Glu Glu His Asp Thr Ser Val Thr Tyr Glu Glu Gly Thr Val Asp			
325	330	335	
Gly Leu Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly			
340	345	350	
Ser Phe Val Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser			
355	360	365	
Gly Asp Cys Thr Arg Gly Thr Thr Tyr Tyr Gln Pro Val Asn Pro			
370	375	380	
Ile Leu Ser Thr Tyr Gly Leu Thr Leu Lys Thr Ser Thr Ala Pro Thr			
385	390	395	400
Asp Thr Pro Ser Asp Pro Val Asp Gln Ser Gly Val Trp Ala Ala Gly			
405	410	415	
Arg Val Tyr Glu Val Gly Ala Gln Val Thr Tyr Ala Gly Val Thr Tyr			
420	425	430	
Gln Cys Leu Gln Ser His Gln Ala Gln Gly Val Trp Gln Pro Ala Ala			
435	440	445	
Thr Pro Ala Leu Trp Gln Arg Leu			
450	455		

<210> 654

<211> 458

<212> PRT

<213> Streptomyces lividans

<400> 654

Met Pro His Arg His Arg His His Arg Ala Val Gly Ala Ala Val Ala			
1	5	10	15
Ala Thr Ala Ala Leu Leu Val Ala Gly Leu Ser Gly Ser Ala Ser Ala			
20	25	30	
Gly Thr Ala Pro Ala Gly Ser Ala Pro Thr Ala Ala Glu Thr Leu Arg			
35	40	45	
Thr Asp Ala Ala Pro Pro Ala Leu Leu Lys Ala Met Gln Arg Asp Leu			
50	55	60	
Gly Ile Asp Arg Arg Gln Ala Glu Arg Arg Leu Val Asn Glu Ala Glu			
65	70	75	80
Ala Gly Ala Thr Ala Gly Arg Leu Arg Ala Ala Leu Gly Gly Asp Phe			
85	90	95	
Ala Gly Ala Trp Val Arg Gly Ala Glu Ser Gly Thr Leu Thr Val Ala			
100	105	110	

Thr Thr Asp Ala Gly Asp Val Ala Ala Val Glu Ala Arg Gly Ala Glu
 115 120 125
 Ala Lys Val Val Arg His Ser Leu Ala Asp Leu Asp Ala Ala Lys Ala
 130 135 140
 Arg Leu Asp Thr Ala Ala Ala Gly Leu Asn Thr Ala Asp Ala Pro Val
 145 150 155 160
 Trp Tyr Val Asp Thr Arg Thr Asn Thr Val Val Val Glu Ala Ile Arg
 165 170 175
 Pro Ala Ala Ala Arg Ser Leu Leu Thr Ala Ala Gly Val Asp Gly Ser
 180 185 190
 Leu Ala His Val Lys Asn Arg Thr Glu Arg Pro Arg Thr Phe Tyr Asp
 195 200 205
 Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg Cys Ser
 210 215 220
 Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala Thr Ala
 225 230 235 240
 Gly His Cys Asp Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn Arg Val
 245 250 255
 Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp Met Ala
 260 265 270
 Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val Leu Gly
 275 280 285
 Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser Pro Val
 290 295 300
 Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
 305 310 315 320
 Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly Thr Ile
 325 330 335
 Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
 340 345 350
 Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly
 355 360 365
 Ser Gly Asp Cys Arg Thr Gly Gly Thr Phe Phe Gln Pro Ile Asn
 370 375 380
 Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly Gly Asp
 385 390 395 400
 Asp Gly Gly Asp Asp Gly Gly Glu Glu Pro Gly Gly Thr Trp Ala
 405 410 415
 Ala Gly Thr Val Tyr Gln Pro Gly Asp Thr Val Thr Tyr Gly Gly Ala
 420 425 430
 Thr Phe Arg Cys Leu Gln Gly His Gln Ala Tyr Ala Gly Trp Glu Pro
 435 440 445
 Pro Asn Val Pro Ala Leu Trp Gln Arg Val
 450 455

<210> 655

<211> 463

<212> PRT

<213> Streptomyces coelicolor A3 (2)

<400> 655

Met Pro His Arg His Arg His His Arg Ala Val Gly Ala Ala Val Ala
 1 5 10 15
 Ala Thr Ala Ala Leu Leu Val Ala Gly Leu Ser Gly Ser Ala Ser Ala
 20 25 30
 Gly Thr Ala Pro Ala Gly Ser Ala Pro Thr Ala Ala Glu Thr Leu Arg

35	40	45
Thr Asp Ala Ala Pro Pro Ala Leu Leu Lys Ala Met Gln Arg Asp Leu		
50	55	60
Gly Leu Asp Arg Arg Gln Ala Glu Arg Arg Leu Val Asn Glu Ala Glu		
65	70	75
Ala Gly Ala Thr Ala Gly Arg Leu Arg Ala Ala Leu Gly Gly Asp Phe		
85	90	95
Ala Gly Ala Trp Val Arg Gly Ala Glu Ser Gly Thr Leu Thr Val Ala		
100	105	110
Thr Thr Asp Ala Gly Asp Val Ala Ala Ile Glu Ala Arg Gly Ala Glu		
115	120	125
Ala Lys Val Val Arg His Ser Leu Ala Asp Leu Asp Ala Ala Lys Ala		
130	135	140
Arg Leu Asp Thr Ala Ala Ala Gly Leu Asn Thr Ala Asp Ala Pro Val		
145	150	155
Trp Tyr Val Asp Thr Arg Thr Asn Thr Val Val Val Glu Ala Ile Arg		
165	170	175
Pro Ala Ala Ala Arg Ser Leu Leu Thr Ala Ala Gly Val Asp Gly Ser		
180	185	190
Leu Ala His Val Lys Asn Arg Thr Glu Arg Pro Arg Thr Phe Tyr Asp		
195	200	205
Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg Cys Ser		
210	215	220
Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala Thr Ala		
225	230	235
Gly His Cys Gly Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn Arg Val		
245	250	255
Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp Met Ala		
260	265	270
Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val Leu Gly		
275	280	285
Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser Pro Val		
290	295	300
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly		
305	310	315
Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly Thr Ile		
325	330	335
Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly		
340	345	350
Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly		
355	360	365
Ser Gly Asp Cys Arg Thr Gly Gly Glu Thr Phe Phe Gln Pro Ile Asn		
370	375	380
Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly Gly Asp		
385	390	395
Asp Gly Gly Asp Asp Gly Gly Asp Asp Gly Gly Glu Glu Pro		
405	410	415
Gly Gly Thr Trp Ala Ala Gly Thr Val Tyr Gln Pro Gly Asp Thr Val		
420	425	430
Thr Tyr Gly Gly Ala Thr Phe Arg Cys Leu Gln Gly His Gln Ala Tyr		
435	440	445
Ala Gly Trp Glu Pro Pro Asn Val Pro Ala Leu Trp Gln Arg Val		
450	455	460

<210> 656
<211> 457
<212> PRT

<213> Streptomyces griseus

<400> 656

Met Glu Arg Thr Thr Leu Arg Arg Arg Ala Leu Val Ala Gly Thr Ala
1 5 10 15
Thr Val Ala Val Gly Ala Leu Ala Gly Leu Thr Gly Val Ala
20 25 30
Ser Ala Asp Pro Ala Ala Thr Ala Ala Pro Pro Val Ser Ala Asp Ser
35 40 45
Leu Ser Pro Gly Met Leu Ala Ala Leu Glu Arg Asp Leu Gly Leu Asp
50 55 60
Glu Asp Ala Ala Arg Ser Arg Ile Ala Asn Glu Tyr Arg Ala Ala Ala
65 70 75 80
Val Ala Ala Gly Leu Glu Lys Ser Leu Gly Ala Arg Tyr Ala Gly Ala
85 90 95
Arg Val Ser Gly Ala Lys Ala Thr Leu Thr Val Ala Thr Thr Asp Ala
100 105 110
Ser Glu Ala Ala Arg Ile Thr Glu Ala Gly Ala Arg Ala Glu Val Val
115 120 125
Gly His Ser Leu Asp Arg Phe Glu Gly Val Lys Lys Ser Leu Asp Lys
130 135 140
Ala Ala Leu Asp Lys Ala Pro Lys Asn Val Pro Val Trp Tyr Val Asp
145 150 155 160
Val Ala Ala Asn Arg Val Val Val Asn Ala Ala Ser Pro Ala Ala Gly
165 170 175
Gln Ala Phe Leu Lys Val Ala Gly Val Asp Arg Gly Leu Val Thr Val
180 185 190
Ala Arg Ser Ala Glu Gln Pro Arg Ala Leu Ala Asp Ile Arg Gly Gly
195 200 205
Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg Cys Ser Val Gly Phe Ser
210 215 220
Val Thr Arg Gly Thr Gln Asn Gly Phe Ala Thr Ala Gly His Cys Gly
225 230 235 240
Arg Val Gly Thr Thr Asn Gly Val Asn Gln Gln Ala Gln Gly Thr
245 250 255
Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp Ile Ala Trp Val Ala Thr
260 265 270
Asn Ala Asn Trp Thr Pro Arg Pro Leu Val Asn Gly Tyr Gly Arg Gly
275 280 285
Asp Val Thr Val Ala Gly Ser Thr Ala Ser Val Val Gly Ala Ser Val
290 295 300
Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Gln
305 310 315 320
Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr Ile Ser Gly Val Thr
325 330 335
Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile
340 345 350
Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys
355 360 365
Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro Ile Asn Pro Leu Leu Gln
370 375 380
Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly Gly Gly Thr Pro Thr Asp
385 390 395 400
Pro Pro Thr Thr Pro Pro Thr Asp Ser Pro Gly Gly Thr Trp Ala Val
405 410 415
Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val Thr Tyr Gly Gly Ala Thr

420 425 430
Tyr Arg Cys Leu Gln Ala His Thr Ala Gln Pro Gly Trp Thr Pro Ala
435 440 445
Asp Val Pro Ala Leu Trp Gln Arg Val
450 455